

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:23:52 ; Search time 11 Seconds
(without alignments)
192.209 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDLGKRLMESHGFE.....MIVECMNNATCTRYIEKVQ 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	100.0	135	10	US-09-788-074-1
2	612	85.8	135	10	US-09-788-074-3
3	380	53.3	132	10	US-09-901-436A-11
4	362	50.8	132	10	US-09-905-235-11
5	333	46.7	132	10	US-09-986-240-2
6	333	46.7	133	10	US-09-901-436A-10
7	333	46.7	133	12	US-10-153-740-13
8	320	44.9	133	12	US-10-153-740-12
9	318	44.6	133	10	US-09-901-436A-7
10	318	44.6	133	12	US-10-153-740-11
11	292	41.0	132	10	US-09-971-187-2
12	280.5	39.3	131	12	US-10-153-740-15
13	219.5	30.8	149	10	US-09-925-302-496
14	214.5	30.1	138	9	US-09-736-457-328
15	193	27.1	160	10	US-09-925-301-848
16	186	26.1	135	10	US-09-901-436A-8
17	184	25.8	135	10	US-09-737-149-48
18	184	25.8	135	12	US-10-153-740-2
19	182	25.5	135	10	US-09-737-149-49

20	181	25.4	135	10	US-09-737-149-16	Sequence 16, Appl
21	150	21.0	134	10	US-09-901-436A-9	Sequence 9, Appl
22	138	19.4	156	10	US-09-737-149-14	Sequence 14, Appl
23	133	18.7	107	10	US-09-901-436A-2	Sequence 2, Appl
24	123.5	17.3	106	12	US-10-153-740-14	Sequence 14, Appl
25	114	16.0	70	10	US-09-737-149-46	Sequence 46, Appl
26	114	16.0	70	10	US-09-737-149-47	Sequence 47, Appl
27	91.5	12.8	997	10	US-09-747-371-3	Sequence 3, Appl
28	83	11.6	614	10	US-09-782-051-2	Sequence 2, Appl
29	76	10.7	26	10	US-09-347-064-14	Sequence 14, Appl
30	73.5	10.3	999	10	US-09-747-371-2	Sequence 2, Appl
31	72	10.1	396	10	US-09-837-751-2	Sequence 2, Appl
32	71	10.0	127	9	US-09-981-353-21	Sequence 21, Appl
33	71	10.0	253	10	US-09-815-242-10279	Sequence 10279, A
34	70	9.8	1426	10	US-09-912-020-340	Sequence 340, App
35	69	9.7	253	10	US-09-815-242-13878	Sequence 13878, A
36	67	9.4	1499	10	US-09-911-826A-2	Sequence 2, Appl
37	66.5	9.3	429	10	US-09-742-954-12	Sequence 12, Appl
38	66.5	9.3	758	10	US-09-903-248-2	Sequence 2, Appl
39	66.5	9.3	758	10	US-09-859-604-2	Sequence 2, Appl
40	66.5	9.3	758	10	US-09-903-063-2	Sequence 2, Appl
41	66.5	9.3	758	10	US-09-903-216-2	Sequence 2, Appl
42	66.5	9.3	758	10	US-09-903-199-2	Sequence 2, Appl
43	66.5	9.3	758	10	US-09-903-023-2	Sequence 2, Appl
44	65.5	9.2	750	10	US-09-402-100-2	Sequence 2, Appl
45	65.5	9.2	832	10	US-09-919-585-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-788-074-1
; Sequence 1, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Holamislil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MALL
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-074-1

Query Match	100.0%	Score 713:	DB 10:	Length 135:
Best Local Similarity	100.0%	Pred No. 2.7e-71:		
Matches 135:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1	MASLKDLGKRLMESHGFEYMKELGVGLARLKMAAMAKPDCIITCDGNNITVKTESTV	60	
Db	1	MASLKDLGKRLMESHGFEYMKELGVGLARLKMAAMAKPDCIITCDGNNITVKTESTV	60	
Qy	61	KTTVFSCNLGKFPDETADGRKTCTTCTODGALVHOHQWDGKRESTITRKLKDGKMIVEC	120	
Db	61	KTTVFSCNLGKFPDETADGRKTCTTCTODGALVHOHQWDGKRESTITRKLKDGKMIVEC	120	
Qy	121	VMNNATCTRYIEKVQ	135	
Db	121	VMNNATCTRYIEKVQ	135	
RESULT 2				
US-09-788-074-3				
; Sequence 3, Application US/09788074				
; Patent No. US20010044110A1				
; GENERAL INFORMATION:				

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: APPLICANT: Hotamisligil, Cokhan S.
: TITLE OF INVENTION: INHIBITION OF MAL1
: FILE REFERENCE: 21509-044
: CURRENT APPLICATION NUMBER: US/09/788,074
: CURRENT FILING DATE: 2001-02-16
: PRIOR APPLICATION NUMBER: 60/183,106
: PRIOR FILING DATE: 2000-02-17
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 135
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-788-074-3

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Query Match	85.9%	Score 612;	DB 10;	Length 135;
Best Local Similarity	80.0%;	Pred. No. 3.2e-60;		
Matches 108;	Conservative 18;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	1	MASLKDLGGKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCITCDGNITVKTESTV	60	
		: : : : : : : : : :		
Db	1	MATVQQLGGRWLRVDSKGFDEYMKELGVGLALRKMGAMAKPDCITCDGKNLTITKTESTL	60	
Qy	61	KTVVFSCNLGKEKPEFTTADGRKKTCTVCTFQDQALVQHQWQDQKESTITRKLKDGKMIVEC	120	
		: : : : : : : : : :		
Db	61	KTTQFSCITLGEKPEFTTADGRKKTCTVCTFQDQALVQHQWQDQKESTITRKLKDGKLVVEC	120	
Qy	121	VMNNATCTRVYEKQV	135	
		: : : : : : : : :		
Db	121	VMNNVTCTRIYEKVE	135	

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RESULT 3
US-09-901-436A-11
, Sequence 11, Application US/09901436A
, Patent No. US20020098515a1
, GENERAL INFORMATION:
, APPLICANT: Ni et al.
, TITLE OF INVENTION: Cytostatin I
, FILE REFERENCE: PF175D4
, CURRENT APPLICATION NUMBER: US/09/901,436A
, CURRENT FILING DATE: 2001-07-10
, PRIOR APPLICATION NUMBER: 09/361,737
, PRIOR FILING DATE: 1999-07-28
, PRIOR APPLICATION NUMBER: 09/023,073
, PRIOR FILING DATE: 1998-02-13
, PRIOR APPLICATION NUMBER: 08/470,298
, PRIOR FILING DATE: 1995-06-06
, PRIOR APPLICATION NUMBER: 08/409,731
, PRIOR FILING DATE: 1995-03-24
, NUMBER OF SEQ ID NOS: 11
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 11
, LENGTH: 132
, TYPE: PRT
, ORGANISM: human
US-09-901-436A-11

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Query Match	53.3%	Score 380;	DB 10;	Length 132;
Best Local Similarity	56.3%;	Pred. No. 9e-35;		
Matches	71;	Conservative 22;	Mismatches 33;	Indels 0; Gaps 0;
QY	9	GKRLMESHGFEFYMKGELGVLALRKKMAAMAKPDCIITCDGNNITVKTTESTVKTTFVFSN	68	
Db		: : : : : : : : : :		
	7	GTWKLVSSENFDDYMKALGVGLATRLGNLAKPVIISKKGDIIITESTFKNTEISFK	66	
QY	69	LGSKFFETTTADGRKTEVTCFFDQALVHQOOWQDGKESTITRKLKDGKMWIECVMNATCT	128	
		: : : : : :		
Db	67	LGQFEFETTTADNRKTSIVTLQRGSLNQVORWDGKETITRKLVLNGKMKVAECKMKGVVCT	126	
QY	129	RYYEKV	134	
		:		
Db	127	RIYEKV	132	

RESULT 4	US-09-90	; Sequen	; Patent	; GENERA	; APPLI	; TITLE	; FILE	; CURRE	; CURRE	; NUMBE	; SOFTW	; SEQ ID	; LENG	; TYPE	; ORGA	US-09-90
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	Query Match	50.8%	Score 362;	DB 10;	Length 132;
	Best Local Similarity	54.4%;	Pred. No. 8.5e-33;		
	Matches	68;	Conservative	22;	Mismatches 35; Indels 0; Gaps 0;
Qy	9	GKWRMLMESHGFEFYMKELGVCLALRKKRAMAKPCIIITCDGNNTVKTSTVTKTVTFVSCN	68		
Dd	7	GTWKLVSSENFDDYMKVEYGVFATRKVAGMAKPNNIISVNGDVTITIKSESTFKNTEISFI	66		
Qy	69	LGEKFDETTADGRKTEVTCTFDQCGLVHQOHWCKGESTITRKLKDGMIVCEVMNNATCT	128		
Dd	67	LGQFEDEVTDADRKKVKSITILDGGLVHVQAWDKGSTIKKRREDDKLVBECVMKGVTST	126		
Qy	129	RVEYK	133		
Dd	127	RYER	131		

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RESULT 5
US-09-986-240-2
; Sequence 2, Application US/09986240
; Patent No. US20020119496A1
; GENERAL INFORMATION:
; APPLICANT: Weigelt, Johan
; APPLICANT: Wikström, Mats
; TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 13425-047001
; CURRENT APPLICATION NUMBER: US/09/986,240
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/243,626
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: SE 0003811-7
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-240-2

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	Query Match	46.7%	Score 333;	DB 10;	Length 132;
	Best Local Similarity	50.4%;	Pred. No. 1.3e-29;		
	Matches 63;	Conservative 23;	Mismatches 39;	Indels 0;	Gaps 0;
Qy	9	GKFLMESHGFEFYKELGVCIALRKRAAMAKPCIIITCDGNNITVKTESIVKTTVFSCN	68		
Db	6	GTWLVDISKFNDDTKMSLGVGFAFRQVASMTPPTIIIEKNGDILTLTHSTFKNTEISFK	65		
Qy	69	LGEKFDETTADGRKTEVCTCFDQGLAQHOQWGDKESTITRKLDDGRKMIVCEVNNATCT	128		
Db	66	LGVEFDETTADDRKVKSVITLDGGLVHLQKWDQGETTLVRELIDGKLLTLTHGTAVCT	125		


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Db      127 RTVEK 131
| |||

RESULT 10
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GEINTEZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-10-153-740-11

Query Match          44.6%; Score 318; DB 12; Length 133;
Best Local Similarity 47.2%; Pred. No. 5.7e-28;
Matches 59; Conservative 27; Mismatches 39; Indels 0; Gaps

Qy 9 GKWLRLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNTIVKTESTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 7 GTWKVLVDKSNFDDYMKSLGVGFATROVASMTKPTTIIKNGDTITIKTQSTFKNTKTEINFQ 66
Qy 69 LGKGFDETTADGRKTEVTVCFFQDGLVGHQWGDGKESTTRKLLKDGKMLVECVMMNATCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 67 LGIEFDEVTADRRKVSLSVTLDDGKGLIHVKWNGQETTLTRELVDGKLLTLTHGSVWST 126
Qy 129 RVYEK 133
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Db 127 RTVEK 131

RESULT 11
US-09-971-187-2
Sequence 2, Application US/09971187

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; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-153-740-15

Query Match          39.3%; Score 280.5; DB 12; Length 131;
Best Local Similarity 44.7%; Pred. No. 7.3e-24;
Matches 55; Conservative 21; Mismatches 46; Indels 1; Gaps 1

QY 11 WRLMESHCFEYMKELGVGLALRMAAAKPDCLITCDGNNITVKTSTVFSCNLG 70
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 9 WKLTNSQNFDEYKALGVGFATRGVNTKPTVIISQEGDKVVIRTLSTFKNTEISFQLG 68
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 71 EKFFETADGRKTVCTVCFQDQALVHOOWDGCKETITRKLKDGKMWCEVNNATCTRV 130
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 69 E-FDETTADDRNCKSVSLDGDGLVHIQKWDGKETNFVREIKDGRKMVTLTFGDVVAVRH 127
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 131 YEK 133
   I I I
Db 128 YEK 130

RESULT 13
US-09-925-302-496
; Sequence 496, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 496
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-496

Query Match          30.8%; Score 219.5; DB 10; Length 149;
Best Local Similarity 35.0%; Pred. No. 4.3e-17;
Matches 48; Conservative 37; Mismatches 45; Indels 7; Gaps 7

QY 2 ASLKDLCKRWLMESHGFEYMKELGVGLARLK--MAAAKPDCLITCDGNNITVKTST 59
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 10 ATMPFSGNWKIIIRSENFEELKVLGVNVMRLKRIAAVAAASKPAVEIKOEGDTFYIKTST 69
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 60 VKTTFVSCNLGKEKFDETTADGRKTVCTVCFQ--DQALVHQH---QWDGKESTIRKL-KDG 114
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 70 VRTTEINFKVEEEREEQIVDGRPCKSLVKWESENKMWCEQKLLKKGEPKTSWTRELTNDG 129
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 115 KMIVCEVNNATCTRVY 131
   I I I
Db 130 ELILMTADDVVCTRVY 146
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I

RESULT 14
US-09-736-457-328
; Sequence 328, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:

```

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; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriack
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-328

Query Match      30.1%; Score 214.5; DB 9; Length 138;
Best Local Similarity 34.8%; Pred. NO. 1.4e-16;
Matches 47; Conservative 36; Mismatches 45; Indels 7; Gaps 4;

QY  4  LKDLGKWLKMGHEEYMKELGVGLALRK--MAAMAKPDCIITCDGNITVKTSTVK 61
DB  1  MFNFGNKKIIRSENFELLKVLGVNVMRLKIAVAASAKPAVEIKOEGDTFYIKTSTVR 60

QY  62  TTVFSCNLGKPDETADGRKTETVCTFQ-DGALVHQH---QWDGKESITIRKL-KDGKM 116
DB  61  TTEINFKVGEEFEQTVDRCPCKSLVKWSENKMYCEQKLLKGEGPKTSWRELNDGEL 120

QY  117  IVECVNNAATCTRVY 131
DB  121  ILTMTADDVVCTRVY 135

RESULT 15
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925.301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-848

Query Match      27.1%; Score 193; DB 10; Length 160;
Best Local Similarity 36.1%; Pred. NO. 3.8e-14;
Matches 44; Conservative 27; Mismatches 45; Indels 6; Gaps 2;

QY  16  SHGFPEYMKELGVGLALRK--MAAMAKPDCIITCDGNITVKTSTVKTVFSCNLGKXF 73
DB  36  SENFDLKLKALGVNAMLRKVAVAASAKPHVEIROQDQDFYIKTSTVTRTEINFKVGEGF 95
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QY  74  DETTADGRKTETVCTFQDGALVHQH---WDGKESITIRKLKGKIMIVECVNNAATCTR 129
DB  96  BEETVDGRKCRSLATWENENKIHCTQTLLLEGDPKTYWTRELANDELILITFGADDDVVCTR 155

QY  130  VY 131
DB  156  IV 157

Search completed: November 25, 2002, 10:25:45
Job time : 12 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:23:07 ; Search time 15 Seconds
(without alignments)
264.806 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDEGKWRMLMESHGFE.....MIVECVNNATCTRVYKQV 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	612	85.8	135	1 US-08-446-600A-4	Sequence 4, Appli
2	380	53.3	132	1 US-08-409-731A-11	Sequence 11, Appl
3	380	53.3	132	2 US-08-470-298B-11	Sequence 11, Appl
4	380	53.3	132	2 US-09-023-073A-11	Sequence 11, Appl
5	380	53.3	132	4 US-09-361-737-11	Sequence 11, Appl
6	333	46.7	133	1 US-08-409-731A-10	Sequence 10, Appl
7	333	46.7	133	2 US-08-470-298B-10	Sequence 10, Appl
8	333	46.7	133	2 US-08-820-825-13	Sequence 13, Appl
9	333	46.7	133	2 US-09-023-073A-10	Sequence 10, Appl
10	333	46.7	133	4 US-09-307-817-13	Sequence 13, Appl
11	333	46.7	133	4 US-09-361-737-10	Sequence 10, Appl
12	333	46.7	133	4 US-09-734-036-13	Sequence 13, Appl
13	320	44.9	133	2 US-08-820-825-12	Sequence 12, Appl
14	320	44.9	133	4 US-09-307-817-12	Sequence 12, Appl
15	320	44.9	133	4 US-09-734-036-12	Sequence 12, Appl
16	318	44.6	131	1 US-08-409-731A-7	Sequence 7, Appli
17	318	44.6	131	2 US-08-470-298B-7	Sequence 7, Appli
18	318	44.6	133	2 US-08-820-825-11	Sequence 11, Appl
19	318	44.6	133	2 US-09-023-073A-7	Sequence 7, Appli
20	318	44.6	133	4 US-09-307-817-11	Sequence 11, Appl
21	318	44.6	133	4 US-09-361-737-7	Sequence 7, Appli
22	318	44.6	133	4 US-09-734-036-11	Sequence 11, Appl
23	292	41.0	132	4 US-09-043-646-2	Sequence 2, Appli
24	280.5	39.3	131	2 US-08-820-825-15	Sequence 15, Appl
25	280.5	39.3	131	4 US-09-307-817-15	Sequence 15, Appl
26	280.5	39.3	131	4 US-09-734-036-15	Sequence 15, Appl
27	271	38.0	132	2 US-08-470-298B-12	Sequence 12, Appl

28	214.5	30.1	138	1	US-08-468-709B-2	Sequence 2, Appli
29	214.5	30.1	138	2	US-08-241-664B-2	Sequence 2, Appli
30	214.5	30.1	138	5	PCT-US93-03936-2	Sequence 4, Appli
31	213	29.9	137	1	US-08-468-709B-4	Sequence 4, Appli
32	213	29.9	137	2	US-08-241-664B-4	Sequence 4, Appli
33	213	29.9	137	5	PCT-US93-03936-4	Sequence 4, Appli
34	210.5	29.5	138	1	US-08-468-709B-12	Sequence 12, Appl
35	210.5	29.5	138	2	US-08-241-664B-12	Sequence 12, Appl
36	210	29.5	137	1	US-08-468-709B-11	Sequence 11, Appl
37	210	29.5	137	2	US-08-241-664B-11	Sequence 11, Appl
38	197.5	27.7	133	1	US-08-554-463-1	Sequence 1, Appli
39	187	26.2	135	1	US-08-409-731A-8	Sequence 8, Appli
40	187	26.2	135	2	US-08-470-298B-8	Sequence 8, Appli
41	187	26.2	135	2	US-08-847-724-4	Sequence 4, Appli
42	186	26.1	135	2	US-08-847-724-6	Sequence 6, Appli
43	186	26.1	135	2	US-09-023-073A-8	Sequence 8, Appli
44	186	26.1	135	3	US-08-899-031-4	Sequence 4, Appli
45	186	26.1	135	4	US-09-361-737-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: NO. 5719126dlund, James J. and Farooqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frost & Jacobs
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
; TELEX: 21-4396 F&J Cin
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; US-08-446-600A-4

Query Match 85.8%; Score 612; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 6.2e-66;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
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Db 1 MATVQLEGRWLRVDSKGEYMKELGVGLALRKMAMAKPDCIITCDGKNLTIKTESTL 60
QY 61 KTVFSCNLCGEKDETTADGRKRTVCTFDGALVQHQWDGKESIITRKLKDGKMIVEC 120
Db 61 KTVFSCNLCGEKEETADGRKRTVCTVCTFDGALVQHQWDGKESIITRKLKDGKLVVEC 120
QY 121 VMNATCTRYEKVQ 135
Db 121 VMNVTCTRIYKVE 135

RESULT 2
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,731A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PFI75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-409-731A-11

Query Match 53.3%; Score 380; DB 1; Length 132;
Best Local Similarity 56.3%; Pred. No. 4, 4e-38;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
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QY 69 LGKEFDETTADGRKRTVCTFDGALVQHQWDGKESIITRKLKDGKMIVECVMNATCT 128
Db 67 LGQEFETADNRKTKSVITLQRLGSLNQVQRWDGKETTITRKLKLVNGKMYAECKMGVCT 126
QY 129 RYVEKV 134
Db 127 RYVEKV 132

RESULT 3
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
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US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PFI75D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
; US-08-470-298B-11

Query Match 53.3%; Score 380; DB 2; Length 132;
Best Local Similarity 56.3%; Pred. No. 4, 4e-38;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLAKEPTVIISKKGDIITRTTESTKNTSEISF 66
QY 69 LGKEFDETTADGRKRTVCTFDGALVQHQWDGKESIITRKLKDGKMIVECVMNATCT 128
Db 67 LGQEFETADNRKTKSVITLQRLGSLNQVQRWDGKETTITRKLKLVNGKMYAECKMGVCT 126
QY 129 RYVEKV 134
Db 127 RYVEKV 132

RESULT 4
US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-409-731A-10

Query Match          46.7%; Score 333; DB 1; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
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QY 69 LGKEFDETTADGRKTTVCTFDDGALVQHQWDGKSESTITRKLKDGKMIKVECMNNATCT 128
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QY 129 RYVEK 133
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Db 127 RYVEK 131

RESULT 7
US-08-470-298B-10
; Sequence 10, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Query Match          46.7%; Score 333; DB 2; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;
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QY 9 GKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
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QY 69 LGKEFDETTADGRKTTVCTFDDGALVQHQWDGKSESTITRKLKDGKMIKVECMNNATCT 128
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Db 67 LGVEFDETTADDRKVKSVITLDGGKLVHLQKWGDGQETTLVRELIDGKLILTLTHGTA VCT 126
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QY 129 RYVEK 133
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Db 127 RYVEK 131

RESULT 8
US-08-820-825-13
; Sequence 13, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-13

Query Match          46.7%; Score 333; DB 2; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
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Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIKNGDILTLKTHSTFKNTEISFK 66
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QY 69 LGKEFDETTADGRKTTVCTFDDGALVQHQWDGKSESTITRKLKDGKMIKVECMNNATCT 128
   ||:|:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~ |:~:~
Db 67 LGVEFDETTADDRKVKSVITLDGGKLVHLQKWGDGQETTLVRELIDGKLILTLTHGTA VCT 126
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QY 129 RYVEK 133
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Db 127 RYVEK 131
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ATTORNEY/AGENT INFORMATION:
NAME: BROOKS ANDERSON

US-08-820-825-12


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Query Match 44.9%; Score 320; DB 2; Length 133;
Best Local Similarity 46.4%; Pred. No. 7.2e-31;
Matches 58; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

Qy 9 CKWRLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRGVNMTPKPTTIIIEVNGDTVIIRKQSTFKNTEISFK 66

Qy 69 LGKEFDETTADGRKTETVCTFQDGLVQHQQWGDGKESTITRKLKDGKMIIVCEVMNATCT 128
Db 67 LGVEFDETTADGRKVSIVTLDDGKLVHVQKWNQGETSLVREWVDGKLILTLTHGTAVCT 126

Qy 129 RVEYK 133
Db 127 RTYEK 131

RESULT 14
US-09-307-817-12
; Sequence 12, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,817
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-817-12

Query Match 44.9%; Score 320; DB 4; Length 133;
Best Local Similarity 46.4%; Pred. No. 7.2e-31;
Matches 58; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

Qy 9 CKWRLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRGVNMTPKPTTIIIEVNGDTVIIRKQSTFKNTEISFK 66

Qy 69 LGKEFDETTADGRKTETVCTFQDGLVQHQQWGDGKESTITRKLKDGKMIIVCEVMNATCT 128
Db 67 LGVEFDETTADGRKVSIVTLDDGKLVHVQKWNQGETSLVREWVDGKLILTLTHGTAVCT 126

Qy 129 RVEYK 133
Db 127 RTYEK 131

RESULT 15
US-09-734-036-12
; Sequence 12, Application US/09734036
; Patent No. 6413726
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-734-036-12

Query Match 44.9%; Score 320; DB 4; Length 133;
Best Local Similarity 46.4%; Pred. No. 7.2e-31;
Matches 58; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

Qy 9 CKWRLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRGVNMTPKPTTIIIEVNGDTVIIRKQSTFKNTEISFK 66

Qy 69 LGKEFDETTADGRKTETVCTFQDGLVQHQQWGDGKESTITRKLKDGKMIIVCEVMNATCT 128
Db 67 LGVEFDETTADGRKVSIVTLDDGKLVHVQKWNQGETSLVREWVDGKLILTLTHGTAVCT 126

Qy 129 RVEYK 133
Db 127 RTYEK 131

Search completed: November 25, 2002, 10:25:28
Job time : 16 secs
```

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:22:52 ; Search time 17 Seconds
(without alignments)
763.420 Million cell updates/sec

Title: US-09-788-074-1

Perfect score: 713

Sequence: 1 MASLKDEGKWRMLMESHGFE.....MIVECVMNATCTRVYEKQ 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	713	100.0	135	2	A47497
2	663	93.0	135	2	JC2201
3	612	85.8	135	2	I56326
4	391	54.8	132	1	MPRB2
5	380	53.3	132	1	MPHU2
6	375	52.6	132	2	S77744
7	369	51.8	132	2	JH0407
8	367	51.5	131	1	MPBO2
9	364	51.1	132	2	S20297
10	362	50.8	132	1	F2HUF
11	357	50.1	132	2	B25952
12	336	47.1	133	2	A27452
13	333	46.7	133	1	F2HUC
14	320	44.9	132	2	I52524
15	320	44.9	133	2	A34676
16	318	44.6	133	2	PC4011
17	308	43.2	132	2	A49184
18	302	42.4	131	2	S06479
19	282	39.6	132	2	I58161
20	282	39.6	132	2	I48923
21	281	39.4	132	2	I56510
22	235.5	33.0	137	2	T25123
23	234.5	32.9	136	2	T15207
24	233.5	32.7	135	2	T15205
25	216.5	30.4	138	2	A42495
26	216.5	30.4	138	2	I51265
27	214.5	30.1	138	1	R3HU2
28	213	29.9	137	1	R3HU1
29	210	29.5	137	1	R3B0A

RESULT 1
A47497
lipid-binding protein, keratinocyte - mouse
N:Alternate names: lipid-binding protein mall
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999
C:Accession: A47497; S36635
R:Krieg, P.; Feil, S.; Fuerstenberger, G.; Bowden, G.T.
J. Biol. Chem. 268, 17362-17369, 1993
A:Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.
A:Reference number: A47497; MUID:93352523; PMID:8349619
A:Accession: A47497
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <R1>
A:Cross-references: EMBL:X70100; NID:g287985; PIDN:CAA49703.1; PID:g287986
C:Superfamily: myelin P2 protein

Query Match 100.0% Score 713; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 7.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLKDEGKWRMLMESHGFEYMKELGVLRLKMAAMAKPDCIITCDGNNITVKTESTV 60
Db 1 MASLKDEGKWRMLMESHGFEYMKELGVLRLKMAAMAKPDCIITCDGNNITVKTESTV 60

QY 61 KTVFVSCNLGEKFDDETTADGRKTETVCTFDGALVQHQWQDGKESTITRKLKDGKMIVEC 120
Db 61 KTVFVSCNLGEKFDDETTADGRKTETVCTFDGALVQHQWQDGKESTITRKLKDGKMIVEC 120

QY 121 VMNATCTRVYEKQ 135
Db 121 VMNATCTRVYEKQ 135

RESULT 2
JC2201
fatty acid-binding protein, cutaneous - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-2000
C:Accession: JC2201; JC7377
R:Watanabe, R.; Fujii, H.; Odani, S.; Sakakibara, J.; Yamamoto, A.; Ito, M.; Ono, T.
Biochem. Biophys. Res. Commun. 200, 253-259, 1994
A:Title: Molecular cloning of a cDNA encoding a novel fatty acid-binding protein from
A:Reference number: JC2201; MUID:94220094; PMID:8166694
A:Accession: JC2201
A:Molecule type: mRNA
A:Residues: 1-135 <WAT>
A:Cross-references: GB:S69874; NID:g546419; PIDN:AAB30574.1; PID:g546420
R:Odani, S.; Namba, Y.; Ishii, A.; Ono, T.; Fujii, H.
J. Biochem. 128, 355-361, 2000

ALIGNMENTS

A:Title: Disulfide bonds in rat cutaneous fatty acid-binding protein.

A:Reference number: JC7377

A:Contents: Skin

A:Accession: JC7377

A:Molecule type: mRNA

A:Residues: 1-135 <ODA>

C:Comment: This protein is involved in intracellular transport and metabolism of fatty acids. This protein, containing two disulfide bonds, is a member of intracellular, l

C:Genetics:

A:Gene: c-fabp

C:Superfamily: myelin P2 protein

C:Keywords: cutaneous gland; disulfide bond; phosphoprotein; skin

F:22/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predicted

F:109/Binding site: fatty acid (Arg) #status predicted

Query Match 93.0%; Score 663; DB 2; Length 135;

Best Local Similarity 91.9%; Pred. No. 5e-57; Indels 0; Gaps 0;

Matches 124; Conservative 6; Mismatches 5;

Qy 1 MASLKDLEGKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60

Db 1 MASLKDLEGKWRMLVESHGFEYMKELGVGLALRKMAAMAKPDCIITLDGNNITVKTESTV 60

Qy 61 KTVFSCNLGKGFDETTADGRKRTVCTFDGALVQHQWDGKESTITRKLKDGKMWVEEC 120

Db 61 KTVFSCNLGKGFDETTADGRKRTVCTFDGALVQHQWDGKESTITRKLKDGKMWVEEC 120

Qy 121 VMNNATCTRVYKVKVQ 135

Db 121 VMNNATCTRVYKVKVQ 135

RESULT 3

I56326

fatty acid binding protein homolog - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I56326

R:Madgen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Celis, J.E.

J. Invest. Dermatol. 99, 299-305, 1992

A:Title: Molecular cloning and expression of a novel keratinocyte protein (psoriasis-ass

ilarity to fatty acid-binding proteins.

A:Reference number: I56326; MUID:92381332; PMID:1512466

A:Accession: I56326

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-135 <RES>

A:Cross-references: GB:M94856; NID:g182353; PIDN:AAA58467.1; PID:g182354

C:Genetics:

A:Gene: PA-FABP

C:Superfamily: myelin P2 protein

Query Match 85.8%; Score 612; DB 2; Length 135;

Best Local Similarity 80.0%; Pred. No. 4.4e-52;

Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MASLKDLEGKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60

Db 1 MATVQQLGKRWRLVDSKGFDEYMKELGVGLALRKMAAMAKPDCIITCDGKMLTINTESTL 60

Qy 61 KTVFSCNLGKGFDETTADGRKRTVCTFDGALVQHQWDGKESTITRKLKDGKMWVEEC 120

Db 61 KTVFSCNLGKGFDETTADGRKRTVCTFDGALVQHQWDGKESTITRKLKDGKMWVEEC 120

Qy 121 VMNNATCTRVYKVKVQ 135

Db 121 VMNNATCTRVYKVKVQ 135

RESULT 4

M9B2

myelin P2 protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999

C:Accession: A28081; A92266; A92372; A03145

R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.

J. Biol. Chem. 263, 8332-8337, 1988

A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.

A:Reference number: A28081; MUID:89228063; PMID:2453513

A:Accession: A28081

A:Molecule type: mRNA

A:Residues: 1-132 <NAR>

A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658

A>Note: translation of Initiator Met is not shown

R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.

J. Biol. Chem. 255, 1058-1063, 1980

A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.

A:Reference number: A92266; MUID:80094496; PMID:7356651

A:Accession: A92266

A:Molecule type: protein

A:Residues: 2-56 <ISI>

R:Ishaque, A.; Hofmann, T.; Eylar, E.H.

J. Biol. Chem. 257, 592-595, 1982

A:Title: The complete amino acid sequence of thr rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423

A:Accession: A92372

A:Molecule type: protein

A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction o

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status predicted

Query Match 54.8%; Score 391; DB 1; Length 132;

Best Local Similarity 57.9%; Pred. No. 1e-30; Indels 0; Gaps 0;

Matches 73; Conservative 22; Mismatches 31;

Qy 9 GKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVTKTVFSCN 68

Db 7 GTWKLVSSSEFDDYMKALGVGLATRLKGLNLAAPNVIIISKKGDIITRTSTFKNTEISFK 66

Qy 69 LGKFEDETTADGRKRTVCTFDGALVQHQWDGKESTITRKLKDGKMWVEECVNNATCT 128

Db 67 LGQFEFETADNRKTKSIITLGERGALVQVQWDGKETTIRKLKLVGKMWVECKMGVVCT 126

Qy 129 RYIEKV 134

Db 127 RYIEKV 132

RESULT 5

MPH02

myelin P2 protein [validated] - human

N:Alternate names: peripheral myelin protein 2

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000

C:Accession: JT0977; A03143; S24224

R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human pe

A:Reference number: JT0977; MUID:92068191; PMID:1720307

A:Accession: JT0977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A>Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98,'N',100-110,'D',112-132 <SUZ>

RESULT 7
JH0407
myelin p2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 13-Aug-1999
C:Accession: JH0407
R:Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 73-80, 1991
A:Title: Structure of the mouse myelin p2 protein gene.
A:Reference number: JH0407; PMID:91268811; PMID:1711100

RESULT 9
S20297
fatty acid-binding protein, hepatic - nurse shark
C:Species: *Ginglymostoma cirratum* (nurse shark)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999
C:Accession: S20297
R:Medzihradszky, K.F.; Gibson, B.W.; Kaur, S.; Yu, Z.; Medzihradszky, D.; Burlingame, Eur. J. Biochem. 203, 327-339, 1992.
A:Title: The primary structure of fatty-acid-binding protein from nurse shark liver.
A:Reference number: S20297; PMID:92137215; PMID:1735421
A:Accession: S20297
A:Molecule type: protein

A:Residues: 1-132 <MED>

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; liver; phosphoprotein

F:1/Modified site: acetylated amino end (Val) #status experimental

Query Match 51.1%; Score 364; DB 2; Length 132;
Best Local Similarity 53.5%; Pred. No. 4.3e-28;
Matches 68; Conservative 21; Mismatches 38; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 68

Db 6 GSWKLOKSHNFDYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 65

QY 69 LGEKDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVCEVMNNATCT 128

Db 66 LAEEFDETTADNRKTKTYKLENGKLVLQVRWDGKSTITRKLKDGKMIIVCEVMNNATCT 125

QY 129 RYVEK 135

Db 126 RYVREQ 132

RESULT 10

F2HUF

fatty acid-binding protein, adipocyte - human

N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein 4

C:Species: Homo sapiens (man)

C:Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999

C:Accession: A33363

R:Baxa, C.A.; Sna, R.S.; Buel, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Boundy

Biochemistry 28, 8683-8690, 1989

A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloning

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

A:Reference number: A33363; MUID:90105397; PMID:2481498

A:Accession: A33363

A:Molecule type: mRNA

A:Residues: 1-132 <BAX>

A:Cross-references: GB:J02874; NID:gl78346; PIDN:AAA51689.1; PID:gl78347

A:Experimental source: subcutaneous fat

C:Genetics:

A:Gene: GDB:FABP4

A:Cross-references: GDB:128030

A:Map position: lp33-lp32

C:Superfamily: myelin P2 protein

C:Keywords: blocked amino end; lipid binding; phosphoprotein

F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #status

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Query Match 50.8%; Score 362; DB 1; Length 132;

Best Local Similarity 54.4%; Pred. No. 6.7e-28;

Matches 68; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 68

Db 7 GTWKLVSSENFDDYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 66

QY 69 LGEKDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVCEVMNNATCT 128

Db 67 LGEKDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVCEVMNNATCT 126

QY 129 RYVEK 133

Db 127 RYVER 131

RESULT 11

myelin P2

N:Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2000

C:Accession: B25952; PC1249; A24884; A05089; A30810; I49440; I49467

R:Phillips, M.; Djian, P.; Green, H.

J. Biol. Chem. 261, 10821-10827, 1986

A:Title: The nucleotide sequence of three genes participating in the adipose differenc

A:Reference number: A92553; MUID:86278164; PMID:3015943

A:Accession: B25952

A:Molecule type: DNA

A:Residues: 1-132 <PHI>

A:Cross-references: GB:M13385; NID:gl98718; PIDN:AAA39417.1; PID:gl387401

A:Note: the authors translated the codon GTG for residue 111 as Gly

R:Bansal, M.P.; Medina, D.

Biochem. Biophys. Res. Commun. 191, 61-69, 1993

A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gl

A:Reference number: PC1248; MUID:93191717; PMID:8447836

A:Accession: PC1249

A:Molecule type: protein

A:Residues: 25-35; 37-51; 59-88 <BAN>

A:Experimental source: mammary gland

R:Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986

A:Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequ

A:Reference number: A24884; MUID:86233319; PMID:3520554

A:Accession: A24884

A:Molecule type: DNA

A:Residues: 1-39,'T',41-110,'G',112-132 <HUN>

A:Cross-references: GB:M13264; NID:g200183; PIDN:AAA39870.1; PID:gl387504

A:Note: the authors translated the codon ACC for residue 40 as Ser

R:Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.

Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984

A:Title: Expression of specific mRNAs during adipose differentiation: identification

A:Reference number: A05089; MUID:84298159; PMID:6208497

A:Accession: A05089

A:Molecule type: mRNA

A:Residues: 1-110,'G',112-132 <BER>

A:Cross-references: GB:K02109; NID:gl98716; PIDN:AAA39416.1; PID:gl293695

R:Matarese, V.; Bernlohr, D.A.

J. Biol. Chem. 263, 14544-14551, 1988

A:Title: Purification of murine adipocyte lipid-binding protein. Characterization as

A:Reference number: A30810; MUID:89008309; PMID:2844775

A:Accession: A30810

A:Molecule type: protein

A:Residues: 2-110,'G',112-132 <MAT>

R:Cook, K.S.; Hunt, C.R.; Spiegelman, B.M.

J. Cell Biol. 100, 514-520, 1985

A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcription

A:Reference number: I49440; MUID:85105214; PMID:3968175

A:Accession: I49440

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 11-110,'G',112-132 <RES>

A:Cross-references: GB:M28726; NID:gl91492; PIDN:AAA37112.1; PID:gl91493

R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988

A:Title: Expression of the differentiation-induced gene for fatty acid-binding protei

A:Reference number: I49467; MUID:88203618; PMID:2452440

A:Accession: I49467

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RE2>

A:Cross-references: GB:M20497; NID:gl91743; PIDN:AAA37188.1; PID:gl91744

A:Experimental source: 3T3-L1 cells

C:Genetics:

C:Superfamily: myelin P2 protein

C:Keywords: lipid binding; phosphoprotein

Query Match 50.1%; Score 357; DB 2; Length 132;

Best Local Similarity 53.6%; Pred. No. 2e-27;

Matches 67; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 68

Db 7 GTWKLVSSENFDDYMKELGVLGALRKMAAMAKPDCTIITCDGNNITVKTSTVKTTFVSCN 66

QY 69 LGEKDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVCEVMNNATCT 128

Db 67 LGVEFEITADDRKRSIIITLDSGALVQKWDGKSTTIKRKEDVDKLVVECVKGTST 126
 QY 129 RYVEK 133
 Db 127 RYVER 131

RESULT 12
 A27452
 fatty acid-binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Dec-1988 #sequence-revision 15-Dec-1988 #text-change 13-Aug-1999
 C:Accession: A28458; A27452; A23838; A39551; A28197; S06478; S02471
 R:Heuckeroth, R.O.; Birkemeyer, E.H.; Levin, M.S.; Gordon, J.I.
 J. Biol. Chem. 262, 9709-9717, 1987
 A:Title: Analysis of the tissue-specific expression, developmental regulation, and linkage
 A:Reference number: A28458; MUID:87250640; PMID:3036869
 A:Accession: A28458
 A:Molecule type: mRNA
 A:Residues: 1-133 <HEU>
 A:Cross-references: GB:J02773; NID:Q204077; PIDN:AAA41136.1; PID:Q204078
 A:Experimental source: cardiac
 R:Clafrey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
 Biochemistry 26, 7900-7904, 1987
 A:Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: 1
 A:Reference number: A27452; MUID:88107756; PMID:3427112
 A:Accession: A27452
 A:Molecule type: mRNA
 A:Residues: 1-133 <CLA>
 A:Cross-references: GB:M18034; NID:Q204079; PIDN:AAA41137.1; PID:Q204080
 A:Experimental source: heart
 R:Sacchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.
 J. Biol. Chem. 261, 8218-8223, 1986
 A:Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocy
 A:Reference number: A23838; MUID:86250713; PMID:2424895
 A:Accession: A23838
 A:Molecule type: protein
 A:Residues: 1-133 <TEK>
 A:Experimental source: heart
 R:Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
 J. Biol. Chem. 266, 5963-5972, 1991
 A:Title: Primary structure and cellular distribution of two fatty acid-binding proteins
 A:Reference number: A39551; MUID:91170283; PMID:2005132
 A:Accession: A39551
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIM>
 A:Experimental source: kidney
 R:Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
 J. Biol. Chem. 263, 4182-4185, 1988
 A:Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by 1
 A:Reference number: A28197; MUID:88153733; PMID:3162235
 A:Accession: A28197
 A:Molecule type: protein
 A:Residues: 2-10; 46-53 <GTB>
 R:Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.; Mut
 Eur. J. Biochem. 185, 27-33, 1989
 A:Title: Purification and characterization of a fatty-acid-binding protein from the gast
 A:Reference number: S06478; MUID:90032682; PMID:2806260
 A:Accession: S06478
 A:Molecule type: protein
 A:Residues: 1-133 <KAN>
 A:Experimental source: stomach
 R:Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.
 Biochem. J. 251, 919-925, 1988
 A:Title: Isolation and characterization of fatty acid binding proteins from mammary tiss
 A:Reference number: S02471; MUID:88326235; PMID:3415652
 A:Accession: S02471
 A:Molecule type: protein
 A:Residues: 16-22; 32-45; 54-59, 'XX', 62-63, 'X', 65-70; 83-93; 97-107; 117-127 <JON>
 A:Experimental source: strain Wistar; mammary

C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotei
 F:133/Product: fatty acid-binding protein #status experimental <MAT>
 F:1/Modified site: acetylated amino end (Met) #status predicted

Query Match 47.1%; Score 336; DB 2; Length 133;
 Best Local Similarity 51.2%; Pred. No. 2.2e-25;
 Matches 64; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGYGLALRKMAAKPKDCITCDGNNTITVKTESTVKTTFVSCN 68
 Db 7 GTWKLVDSKNFDDYMKSLGVGFATQVAVSWTKPTTIIIEKNGDITIKTHSTFNTLSFQ 66
 QY 69 LSGKFDETTADGRKTTFTVCFQDQCALVQHQWDGKSTITRKLKDGKMIIVECVNNATCT 128
 Db 67 LGVEFDEVTADDRKRSVVTLDGGLVQKWDGQETTLTRELSGDKLILTLTHGNVST 126
 QY 129 RYVEK 133
 Db 127 RYVEK 131

RESULT 13
 FZHUO
 fatty acid-binding protein, cardiac and skeletal muscle - human
 N:Alternate names: fatty acid-binding protein 3 (FABP3)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1991 #sequence-revision 03-May-1996 #text-change 16-Jul-1999
 C:Accession: S15432; JH0199; S00603; I54275; A27248
 R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
 Biochem. J. 276, 203-207, 1991
 A:Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protei
 A:Reference number: S15432; MUID:91248148; PMID:1710107
 A:Accession: S15432
 A:Molecule type: mRNA; protein
 A:Residues: 1-133 <PEE>
 A:Cross-references: EMBL:X56549; NID:g31292; PIDN:CAA39889.1; PID:g31293
 A:Experimental source: heart muscle; skeletal muscle
 R:Boerchers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
 Mol. Cell. Biochem. 98, 127-133, 1990
 A:Title: Revision of the amino acid sequence of human heart fatty acid-binding protei
 A:Reference number: JH0199; MUID:91094793; PMID:2266954
 A:Accession: JH0199
 A:Molecule type: protein
 A:Residues: 2-129, 'Q', 131-133 <BOE>
 R:Offner, G.D.; Brecher, P.; Sawilivich, W.B.; Costello, C.E.; Troxler, R.F.
 Biochem. J. 252, 191-198, 1988
 A:Title: Characterization and amino acid sequence of a fatty acid-binding protein fro
 A:Reference number: S00603; MUID:88339792; PMID:3421901
 A:Accession: S00603
 A:Molecule type: protein
 A:Residues: 2-104, 'K', 106-124, 'S', 126-133 <OFF>
 A:Note: submitted to the Protein Sequence Database, May 1988
 R:Zanotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
 J. Biol. Chem. 267, 18541-18550, 1992
 A:Title: Three-dimensional structure of recombinant human muscle fatty acid-binding p
 A:Reference number: A49251; MUID:92406763; PMID:1526991
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms
 A:Note: recombinant protein expressed in Escherichia coli
 R:Troxler, R.F.; Offner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Mlunsky, A.; Wyan
 Hum. Genet. 92, 563-566, 1993
 A:Title: Localization of the gene for human heart fatty acid binding protein to chrom
 A:Reference number: I54275; MUID:94085953; PMID:8262516
 A:Accession: I54275
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 15-133 <RES>
 A:Cross-references: GB:S67314; NID:9458861; PIDN:AAB29294.1; PID:9458862
 C:Genetics:
 A:Gene: GDB:FABP3
 A:Cross-references: GDB:128008; OMIM:134651
 A:Map position: lp33-tp32
 C:Superfamily: myelin p2 protein

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:19:37 ; Search time 36 Seconds
(without alignments)
499.690 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKLEKRWLMESHGFE.....MIVECVMNNTCTRYEYKQ 135

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	100.0	135	AAU08673	Mouse keratinocyte
2	617	86.5	146	ABG60208	Human D17HP polype
3	612	85.8	135	AAR55866	Melanogenic inhibi
4	612	85.8	135	AAU08674	Human keratinocyte
5	603	84.6	158	ABG27577	Novel human diagno
6	599	84.0	135	ABG61772	Novel fatty acid-b
7	535.5	75.1	134	AAU08666	Human NOV10 protein
8	530.5	74.4	163	AAU08665	Human NOV9 protein
9	387.5	54.3	172	AAU10059	Fatty acid-binding
10	372.5	52.2	181	ABG13617	Novel human diagno

11	368	51.6	136	19	AAW40227	Human myelin P2 pr
12	362	50.8	132	21	AAV90320	Human AFABP protei
13	362	50.8	132	23	ABB08076	Human ap2 protein.
14	359	50.4	132	21	AAV90319	Mouse AFABP protei
15	356	49.9	136	19	AAW40228	Bovine myelin P2 p
16	333	46.7	133	22	AAG66578	Human MDGI polypep
17	330	46.3	131	12	AAR13559	MDGI active peptid
18	320.5	45.0	134	18	AAW31534	Porcine heart-fatt
19	320	44.9	133	22	AAG66577	Mouse MDGI polypep
20	318	44.6	133	22	AAG66576	Mouse MDGI polypep
21	293	41.1	117	21	AAW3847	Human secreted pro
22	292	41.0	132	18	AAW22408	Human cytostatin I
23	292	41.0	132	19	AAW80949	Amino acid sequenc
24	292	41.0	132	19	AAW81106	Human cytostatin I
25	292	41.0	132	20	AAW82403	Human 14-16 kDa FA
26	282	39.6	132	16	AAW75423	Mouse cellular X b
27	280.5	39.3	131	22	AAG66580	Human cytostatin I
28	280	39.3	132	21	AAW3957	Human secreted pro
29	257.5	36.1	130	22	ABG62690	Drosophila melanog
30	228	32.0	522	22	ABG13615	Novel human diagno
31	219.5	30.8	149	21	AAW58158	Lung cancer associ
32	214.5	30.1	138	14	AAW42211	CRABP-II gene prod
33	214.5	30.1	138	22	AAW76852	Human lung tumour
34	214.5	30.1	138	23	AAW85507	Clone #19122 of lu
35	213	29.9	137	14	AAW42212	CRABP-I gene produ
36	205.5	28.8	132	22	AAU10065	Cytostatin family
37	205.5	28.8	135	22	AAU10066	Cytostatin family
38	205.5	28.8	433	22	ABG27578	Novel human diagno
39	200.5	28.1	117	22	AAU30142	Novel human secret
40	197.5	27.7	133	16	AAW75643	Schistosoma manso
41	196	27.5	82	22	AAG75123	Human colon cancer
42	196	27.5	88	21	AAW58740	Breast and ovarian
43	193	27.1	160	21	AAW43403	Human cancer assoc
44	186	26.1	219	23	ABP41914	Human ovarian anti
45	184	25.8	135	18	AAW30891	Human cytostatin I

ALIGNMENTS

RESULT 1
AAU08673
ID AAU08673 standard; Protein; 135 AA.
XX AAU08673;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse keratinocyte fatty acid binding protein, Mall.
XX
KW Mouse; Mal 1; keratinocyte fatty acid binding protein; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX
XX Mus musculus.
XX
XX WO200160384-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US05019.
XX
PR 17-FEB-2000; 2000US-0183106.
XX (HARD) HARVARD COLLEGE.
XX Hotamisligil GS;
XX
DR WPI: 2001-570550/64.
DR N-PSDB; AAS13246.
XX
PT Reducing the level of circulating free fatty acids in a mammal, useful
PT for treating or preventing obesity, diabetes, dyslipidaemia or

PT atherosclerosis, by administering a keratinocyte lipid binding protein
PT inhibitor
XX
PS Disclosure; Page 2; 27pp; English.
XX
CC The invention relates to reducing the level of circulating free fatty
CC acids in a mammal comprising administering to a mammal a compound that
CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
CC fatty acid binding protein) or Mall activity. The method is useful for
CC reducing the level of circulating free fatty acids in a mammal,
CC particularly in a mammal that is suffering from or at risk of developing
CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
CC useful for diagnosing these diseases. The present sequence is Mouse
CC Mal 1.
XX
SQ Sequence 135 AA:
Query Match 100.0%; Score 713; DB 22; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLKDLEKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
Db 1 MASLKDLEKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
QY 61 KTVFSCNLGKGFDETTADGRKTTVCTFDGALVHQHQWQDCKESTITRKLKDGKMWVVC 120
Db 61 KTVFSCNLGKGFDETTADGRKTTVCTFDGALVHQHQWQDCKESTITRKLKDGKMWVVC 120
QY 121 VMNNATCTRVYKQV 135
Db 121 VMNNATCTRVYKQV 135
RESULT 2
ID ABG60208 standard; Protein; 146 AA.
XX
AC ABG60208;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human DITHP polypeptide #266.
XX
KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW thymus.
XX
OS Homo sapiens.
XX
PN WO200220754-A2.
XX
PD 14-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27127.
XX
PR 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230583P.
PR 06-SEP-2000; 2000US-230588P.
PR 06-SEP-2000; 2000US-230514P.
PR 06-SEP-2000; 2000US-230515P.
PR 06-SEP-2000; 2000US-230517P.
PR 06-SEP-2000; 2000US-230518P.
PR 06-SEP-2000; 2000US-230519P.

PR 06-SEP-2000; 2000US-230595P.
PR 06-SEP-2000; 2000US-230597P.
PR 06-SEP-2000; 2000US-230598P.
PR 06-SEP-2000; 2000US-230599P.
PR 06-SEP-2000; 2000US-230610P.
PR 06-SEP-2000; 2000US-230655P.
PR 06-SEP-2000; 2000US-230988P.
PR 07-SEP-2000; 2000US-230951P.
PR 07-SEP-2000; 2000US-231163P.
PR 07-SEP-2000; 2000US-231167P.
XX (INCY-) INCYTE GENOMICS INC.
PA Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
XX Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
DR N-PSDB; ABK71797.
XX
PT An isolated polynucleotide useful in diagnostics and therapeutics -
XX
PS Claim 29; Page 679; 686pp; English.
XX
CC The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
XX
SQ Sequence 146 AA:
Query Match 86.5%; Score 617; DB 23; Length 146;
Best Local Similarity 86.9%; Pred. No. 2.3e-63;
Matches 119; Conservative 8; Mismatches 8; Indels 2; Gaps 2;
QY 1 MASLKDLEKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
Db 6 MASLKDLEKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITLDGNNITVKTSTV 65
QY 61 KTVFSCNLGKGFDETTADGRKTTVCTFDGALVHQHQWQDCKESTITRKLKDGKMWVVC 120
Db 66 KTVFSCNLGKGFDETTADGRKTTVCTFDGALVHQHQWQDCKESTITRKLKDGKMWVVC 125
QY 121 VMNNA-TCTR-VYKQV 135
Db 126 VMNCPCTSGLMTKVQ 142
RESULT 3
ID AAR55866
XX AAR55866 standard; Protein; 135 AA.
AC AAR55866;
XX
DT 07-DEC-1994 (first entry)
XX
DE Melanogenic inhibitor.
XX
KW Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;

KW depigmentation; melanoma.
 XX OS Homo sapiens.
 XX PN W09412534-A.
 XX PD 09-JUN-1994.
 XX PF 16-NOV-1993; 93WO-US11139.
 XX PR 24-NOV-1992; 92US-0980513.
 XX PR 01-SEP-1993; 93US-0115172.
 XX PA (UYCI-) UNIV CINCINNATI.
 XX PI Faroocqui JZ, Nordlund JJ;
 XX DR WPI: 1994-200198/24.
 XX DR N-PSDB; AAQ66842.
 XX PT Prodn. of a protein for inhibiting melanogenesis - useful for
 PT treating hyper-pigmentary diseases, destroying melanoma cells and
 PT for lightening unwanted body hair
 XX PS Disclosure; Page 5; 40pp; English.
 XX CC PCR primers given in AAQ66843-44 were used to amplify RNA from
 CC human skin previously grafted onto nude mice, thereby providing
 CC DNA (AAQ66842) encoding melanogenic inhibitor protein (AAR55866).
 XX SQ Sequence 135 AA;
 Query Match 85.8%; Score 612; DB 15; Length 135;
 Best Local Similarity 80.0%; Pred. No. 7.9e-63;
 Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MASLKDEKRWLMESHGFEYMKELGVGLALRKKMAAMAKPDCIITCDGNNITVKTESTV 60
 Db 1 MATVQOLEGRLVDSKGFDEYMKELGVGLALRKKMGAMAKPDCIITCDGKNLTIKTESTL 60
 QY 61 KTVFSCNLGKXFDETTADGRKTETVCTFDGALVQHQWQDGKKESTITRKLKDGKMIVEC 120
 Db 61 KTFQFCTLGEKFEETADGRKTQTVCNFTDGLVQHQEWQDGKKESTITRKLKDGKLVVEC 120
 QY 121 VMNNATCTRYEKVQ 135
 Db 121 VMNNVTCTRIYEKVE 135
 RESULT 4
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 DT 18-DEC-2001 (first entry)
 DE Human keratinocyte fatty acid binding protein, Mall.
 XX KW Human; Mal 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antisenese therapy.
 XX OS Homo sapiens.
 XX PN W0200160384-A1.
 XX PD 23-AUG-2001.
 XX PF 16-FEB-2001; 2001WO-US05019.
 XX PR 17-FEB-2000; 2000US-0183106.

PA (HARD) HARVARD COLLEGE.
 XX PI Hotamisliligil GS;
 XX DR WPI: 2001-570550/64.
 XX DR N-PSDB; AAS13247.
 XX PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor
 XX PS Disclosure; Page 2; 27pp; English.
 XX CC The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
 CC fatty acid binding protein) or Mall activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
 CC useful for diagnosing these diseases. The present sequence is Human
 CC Mal 1.
 XX SQ Sequence 135 AA;
 Query Match 85.8%; Score 612; DB 22; Length 135;
 Best Local Similarity 80.0%; Pred. No. 7.9e-63;
 Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MASLKDEKRWLMESHGFEYMKELGVGLALRKKMAAMAKPDCIITCDGNNITVKTESTV 60
 Db 1 MATVQOLEGRLVDSKGFDEYMKELGVGLALRKKMGAMAKPDCIITCDGKNLTIKTESTL 60
 QY 61 KTVFSCNLGKXFDETTADGRKTETVCTFDGALVQHQWQDGKKESTITRKLKDGKMIVEC 120
 Db 61 KTFQFCTLGEKFEETADGRKTQTVCNFTDGLVQHQEWQDGKKESTITRKLKDGKLVVEC 120
 QY 121 VMNNATCTRYEKVQ 135
 Db 121 VMNNVTCTRIYEKVE 135
 RESULT 5
 ID ABG27577 standard; Protein; 158 AA.
 AC ABG27577;
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #27568.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN W0200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 XX DR N-PSDB; AAS91764.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 57936; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABC00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 158 AA;

Query Match 84.6%; Score 603; DB 22; Length 158;
Best Local Similarity 79.3%; Pred. No. 1.1e-61;
Matches 107; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 MASLKDLEKWRMLSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
DB 24 MATVQLEGRWRLLVDSKGFDEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTL 83
QY 61 KTVFSCNLGKFEFTADGRKTEVCTFDGALVQHQWQDCKESTITRKLKDGKLVVEC 120
DB 84 KTFQFSCNLGKFEFTADGRKTEVCTFDGALVQHQWQDCKESTITRKLKDGKLVVEC 143
QY 121 VMNNATCTRYEKVQ 135
DB 144 VMNNATCTRYEKVE 158

RESULT 6
ABG61772
ID ABG61772 standard; Protein; 135 AA.

XX ABG61772;

XX 14-AUG-2002 (first entry)

DE Novel fatty acid-binding protein-like protein.

XX Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;
KW behavioral disorder; valve disease; endocrine disorder; heart disorder;
KW blood disorder; anxiety disorder; brain disorder; inflammatory disorder;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
KW gene therapy; transgenic animal; human.

OS Homo sapiens.

XX WO200229058-A2.

XX 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31248.
XX
PR 05-OCT-2000; 2000US-238323P.
PR 05-OCT-2000; 2000US-238325P.
PR 06-OCT-2000; 2000US-238372P.
PR 06-OCT-2000; 2000US-238373P.
PR 06-OCT-2000; 2000US-238379P.
PR 06-OCT-2000; 2000US-238382P.
PR 06-OCT-2000; 2000US-238383P.
PR 06-OCT-2000; 2000US-238384P.
PR 06-OCT-2000; 2000US-238397P.
PR 06-OCT-2000; 2000US-238400P.
PR 06-OCT-2000; 2000US-238401P.
PR 06-OCT-2000; 2000US-238402P.
PR 14-MAR-2001; 2001US-275892P.
PR 08-JUN-2001; 2001US-296860P.
XX
PA (CURA-) CURAGEN CORP.

XX ShmKets RA, Taupier RJ, Burgess CE, Zerhusen BD, Mezes PS;
PI Rastelli L, Malvankar UM, Grosse WM, Alsobrook JP, Lepley DM;
PI Spytek KA, Li L, Edinger S, Gerlach V, Ellerman K, Macdougall J;
PI Gunther E, Millet I, Stone D, Smithson G, Szekeres ES;
XX
DR WPI; 2002-444103/47.
DR N-PSDB; ABK92039.

XX Novel isolated polypeptide, designated NOVX, useful for treating or
PT preventing cancer, diabetes, obesity, dyslipidaemia, anorexia, and
PT metabolic, neurodegenerative, immune and hematopoietic disorders -
XX
PS Claim 1; Page 42; 316pp; English.

XX The invention describes an isolated polypeptide (I), useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease. (I), the polynucleotide encoding it (II) and an antibody
CC (III) to (I) are useful for treating or preventing cancer, metabolic
CC disorders, skin disorders, infectious disease, anorexia, behavioral
CC disorders, valve diseases, endocrine disorders, heart and blood
CC disorders, anxiety disorders, brain disorders, inflammatory disorders,
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, and the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases. (I), (II) or (III) are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g., diagnostic assays and prognostic assays), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) is
CC useful as immunogen to produce antibodies immunospecific for (I), to
CC screen for potential agonist and antagonist compounds, and as bait
CC protein in a two-hybrid or three-hybrid assay. (II) is useful in gene
CC therapy, to express (I), to detect (I) mRNA or a genetic lesion in a (I)
CC gene, and to modulate activity of (I). A cell containing a vector
CC expressing (I) is useful for producing non-human transgenic animals.
CC This is the amino acid sequence of a novel human polypeptide described
CC in the invention.

XX Sequence 135 AA;

Query Match 84.0%; Score 599; DB 23; Length 135;
Best Local Similarity 77.8%; Pred. No. 2.5e-61;
Matches 105; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

QY 1 MASLKDLEKWRMLSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
DB 1 MATVQLEGRWRLLVDSKGFDEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTL 60
QY 61 KTVFSCNLGKFEFTADGRKTEVCTFDGALVQHQWQDCKESTITRKLKDGKLVVEC 120
DB 61 KTFQFSCNLGKFEFTADGRKTEVCTFDGALVQHQWQDCKESTITRKLKDGKLVVEC 120
QY 121 VMNNATCTRYEKVQ 135
XX
XX

XX PS Claim 9; Page 34; 128pp; English.

XX CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and

XX CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides

XX CC and anti-NOVX antibodies are useful for treating or preventing a

XX CC pathology associated with NOVX polypeptide in humans and for treating a

XX CC syndrome associated with human disease e.g. disorders characterised by

XX CC altered cell motility, proliferation and migration e.g. cancer,

XX CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.

XX CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's

XX CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,

XX CC asthma, hypertension and seizure (NOV4), enamel defects, such as

XX CC amelogenesis imperfecta and disorders involving enamel defects,

XX CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic

XX CC neurological disorders, e.g. paraneoplastic limbic of brain-stem

XX CC encephalitis occurring during testicular cancer, diabetes, reproductive

XX CC health, metabolic and endocrine disorders, gastrointestinal disorders,

XX CC immune disorders and autoimmune diseases, respiratory disorders, bone

XX CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell

XX CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and

XX CC atherosclerosis, abdominal aortic aneurysm and neurological disorders

XX CC (NOV11). NOVX polypeptide is also useful for identifying an agent that

XX CC binds to it and a cell expressing NOVX polypeptide is useful for

XX CC identifying a therapeutic agent for use in treatment of a NOVX related

XX CC pathology. The antibodies and a polypeptide having 95% sequence identity

XX CC to NOVX polypeptide are useful for treating a pathological state in a

XX CC mammal. The present sequence represents NOV9, a possible epidermal

XX CC fatty acid-binding protein family member.

XX SQ Sequence 163 AA;

Query Match 74.4%; Score 530.5; DB 22; Length 163;
 Best Local Similarity 70.9%; Pred. No. 2.8e-53;
 Matches 95; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 2 ASLKDLQKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNTTVKTESTVK 61
 Db 31 ATVOQLQGRWRLADSKGFDAYMKKLGVLGSLRNMGAMAKPDCIITCDGNNTTVKTESTVK 90
 OY 62 TTVFSCNLGERFDETDAGRTKTEVCTFDGALVHOHQWGDKESTITRKLKDGKIVCEV 121
 Db 91 TTFQFCTLGERFEGTAVGRKTQTVCSFTDGLVPHQEWGDKENTITRKLKDGAS-VVDCV 149
 OY 122 MNATCTRVYKQV 135
 Db 150 TNNVTCTRIYKVE 163

RESULT 9
 AAU10059
 ID AAU10059 standard; Protein; 172 AA.

XX AC AAU10059;

XX DT 14-FEB-2002 (first entry)

XX DE Fatty acid-binding family associated protein, NOV2.

XX NOV; cytostatic; psoriasis; neurotropic; neuroprotectant;
 KW cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;
 KW haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;
 KW differentiation; proliferation; haematopoiesis; wound healing;
 KW angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;
 KW ischaemic injury; neuropathological disorder; skeletal dysplasia;
 KW fatty acid-binding protein; FAPP; chromosome 5.

XX OS Homo sapiens.

XX PN WO200170978-A2.

XX PD 07-SEP-2001.

XX

20-MAR-2001; 2001WO-US09093.

20-MAR-2000; 2000US-190768P.

20-MAR-2000; 2000US-190835P.

22-MAR-2000; 2000US-190972P.

22-MAR-2000; 2000US-191199P.

24-MAR-2000; 2000US-191947P.

28-MAR-2000; 2000US-192657P.

28-MAR-2000; 2000US-192664P.

28-MAR-2000; 2000US-192665P.

28-MAR-2000; 2000US-192984P.

29-MAR-2000; 2000US-192836P.

(CURA-) CURAGEN CORP.

Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;

Vernet CAM;

WPI; 2001-639127/73.

N-PSDB; AAS15722.

polypeptides and nucleic acids related to chloride channel,
 insulin-like growth factor family of proteins, useful for diagnosing
 and treating cancer, cystic fibrosis, acute pancreatitis and
 Alzheimer's disease -

Claim 1; Page 11; 151pp; English.

The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX
 polypeptides are useful for treating pathology associated with NOVX
 polypeptide, determining the presence of or predisposition to a disease
 associated with altered levels of NOVX, identifying agents binding to
 NOVX and treatment of disorders associated with altered expression of
 members of chloride channel-associated proteins e.g. cystic fibrosis and
 congenital myotonia. NOVX proteins are useful in treatment of disorders
 including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
 e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
 in one or more organs (e.g. haemophilia, anaemia), Pendred syndrome,
 skeletal dysplasias, disorders characterised by altered cell shape,
 motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
 disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
 treatment of disorders of vascular smooth muscle cell differentiation,
 (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
 useful to screen for molecules which inhibit or enhance NOVX activity or
 function and are useful as targets for the identifying small molecules,
 that modulate or inhibit e.g. neurogenesis, proliferation, motility,
 cell differentiation, haematopoiesis, wound healing and angiogenesis. NOV
 sequences are also useful for: identifying a cell or tissue type in a
 biological sample; amplifying DNA sequences from very small biological
 samples e.g. hair or skin or body fluids and as primers and probes to
 identify and/or clone NOVX homologues. NOVX proteins are useful
 immunogens to generate antibodies to monitor protein levels and modulate
 NOVX activity. Cells comprising the nucleic acids are useful for
 producing transgenic animals, for studying the function and/or activity
 of NOVX protein and identifying and/or evaluating modulators of NOVX
 protein activity. This sequence is the NOV2 amino acid sequence (the gene
 is located on chromosome 5) related to the fatty acid-binding protein
 family proteins, one of 12 NOV polypeptides described in the method of
 the invention.

Sequence 172 AA;

Query Match 54.3%; Score 387.5; DB 22; Length 172;
 Best Local Similarity 58.0%; Pred. No. 1.1e-36;
 Matches 80; Conservative 22; Mismatches 31; Indels 5; Gaps 4;

OY 1 MASLKDLQKRWLMESHGFEY--YMKELGVGLAL-RKMAAMAKPDCIITCDGNNTTVKTE 57

Db 37 MDTVOQLQGRWRLADSKGFDENKYNKELGVGLALCEKKGAMAKKDCIFFDGNNTTVKTE 96

OY 58 STVKTTFVFCNLGERFDETDAGRTKTEVCTFDGALVHOHQWGDKESTITRKLKDGKMI 117

Db 117 STVKTTFVFCNLGERFDETDAGRTKTEVCTFDGALVHOHQWGDKESTITRKLKDGKMI 117

Db 127 RYER 131
||||:

RESULT 14
AA90319
ID AAY90319 standard; Protein; 132 AA.

XX AAY90319;

XX 22-NOV-2000 (first entry)

XX Mouse AFABP protein sequence.

XX AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
XX lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
XX serum cholesterol; therapy; mouse.

XX Mus sp.

XX WO200047734-A1.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03560.

XX 12-FEB-1999; 99US-0119880.

XX (HARD) HARVARD COLLEGE.

XX Lee M, Perrella MA, Hotamisligil GS;

XX WPI; 2000-506094/45.

XX N-PSDB; AAA37716.

XX Reducing expression of adipocyte fatty acid binding protein through
XX administration of a compound is used to inhibit formation of an
XX atherosclerotic lesion -

XX Disclosure: Page 14; 43pp; English.

XX This sequence represents the mouse AFABP (adipocyte fatty
XX acid binding protein) protein sequence. The invention relates to a method
XX for inhibiting formation of an atherosclerotic lesion comprising
XX administering to a mammal a compound that reduces expression of adipocyte
XX fatty acid binding protein (AFABP). The method is used to inhibit
XX formation of atherosclerotic lesions. The method is used to identify
XX compounds which can be used to inhibit formation of atherosclerotic
XX lesions through inhibition of AFABP binding to an intracellular ligand
XX in a macrophage or adipocyte, inhibition of development of an
XX atherosclerotic lesion, inhibition of a macrophage differentiating into
XX a foam cell or inhibition of AFABP expression in a cell. AFABP activity
XX may be inhibited to treat atherosclerosis or to treat individuals at risk
XX of developing atherosclerosis. Inhibiting AFABP expression or activity
XX reduces the development of atherosclerotic lesions despite a high level
XX of serum cholesterol.

XX Sequence 132 AA;

Query Match 50.4%; Score 359; DB 21; Length 132;
Best Local Similarity 53.6%; Pred. No. 1.6e-33;
Matches 67; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFBEYMKELGVLALRKKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

Db 7 GTWKLVSSSEFDDYMKVEGVGATRKVAGAKPMIISVNGDLVTRSESTFKNTEISFK 66

QY 69 LGKEFDETTADGRKTTCTVTFDQGVQHQWQDGEKSTITRKLKDGKMIVECVMMNATCT 128

Db 67 LGVFEDEITADGRKVKSIITLDGVALVQVQKWDGKSTTIKRRDGDGLVVECVMKGVTS 126

QY 129 RYER 133

||||:

Db 127 RYER 131

RESULT 15
AAW40228
ID AAW40228 standard; Protein; 136 AA.

XX AAW40228;

XX 26-JUN-1998 (first entry)

XX Bovine myelin P2 protein.

XX Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
XX Guillain-Barre syndrome; vasculitis; nerve inflammation;
XX gammopathy.

XX Bos taurus.

XX WO9803647-A2.

XX 29-JAN-1998.

XX 18-JUL-1997; 97WO-DE01535.

XX 18-JUL-1996; 96DE-1029095.

XX (GOLD/) GOLD R.

XX (WEIS/) WEISHAUP T A.

XX Gold R, Weishaupt A;

XX WPI; 1998-120772/11.

XX Recombinant myelin proteins for treating T-cell mediated disease of
XX peripheral nervous system - by high dose antigen therapy, causing
XX apoptosis in T cells, for treating e.g. polyneuritis or
XX Guillain-Barre syndrome

XX Disclosure: Fig 4; 14pp; German.

XX The present sequence is the bovine myelin P2 protein, which can
XX be used to treat T-cell mediated diseases of the peripheral nervous
XX system, especially chronic-inflammatory polyneuritis,
XX Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
XX of gammopathy.

XX Sequence 136 AA;

Query Match 49.9%; Score 356; DB 19; Length 136;
Best Local Similarity 54.0%; Pred. No. 3.6e-33;
Matches 67; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFBEYMKELGVLALRKKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

Db 7 GTWKLVSSSEFDDYMKVEGVGATRKVAGAKPMIISVNGDLVTRSESTFKNTEISFK 66

QY 69 LGKEFDETTADGRKTTCTVTFDQGVQHQWQDGEKSTITRKLKDGKMIVECVMMNATCT 128

Db 67 LGQEFDETTADNRKTKSTVTLARGLNQVQKWDGNETTIKRLKLVNGKVMVECKMKDVCT 126

QY 129 RYER 132

Db 127 RYED 130

Search completed: November 25, 2002, 10:23:46
Job time : 37 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:22:32 ; Search time 31 Seconds
(without alignments)
897.302 Million cell updates/sec

Title: US-09-788-074-1

Perfect score: 713

Sequence: 1 MASLKDLGKRLMESHGFE.....MIVECVMNATCTRYEKVQ 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	53.7	132	13 Q90X55	Q90X55 gallus gall
2	371	52.0	132	13 Q8QHA8	Q8QHA8 anser anser
3	351	49.2	132	11 Q3DAK4	Q3DAK4 mus musculus
4	333	46.7	150	11 Q9R290	Q9R290 rattus norv
5	331	46.4	113	6 Q9XSG4	Q9XSG4 oryctolagus
6	331	46.4	132	13 Q90W92	Q90W92 fundulus he
7	329	46.1	132	11 Q9DAL2	Q9DAL2 mus musculus
8	317	44.5	125	6 Q9XS15	Q9XS15 equus caball
9	309.5	43.4	134	13 Q57691	Q57691 cryodracro a
10	308.5	43.3	134	13 Q57665	Q57665 gobionototh
11	308	43.2	135	13 Q91896	Q91896 anguilla ja
12	307.5	43.1	134	13 Q57666	Q57666 paracheaenic
13	305.5	42.8	134	13 Q57663	Q57663 notiothenia
14	301	42.2	132	13 Q918N9	Q918N9 brachydanio
15	299	41.9	133	13 Q8UVG7	Q8UVG7 brachydanio
16	289	40.5	136	5 Q8WR15	Q8WR15 metapenaeus

17	283	39.7	99	6	O97675	O97675 sus scrofa
18	283	39.7	133	13	O57668	O57668 cryodracro a
19	282	39.6	133	13	O57667	O57667 chaenoccephala
20	282	39.6	133	13	O57670	O57670 gobionototh
21	281	39.4	133	13	O57669	O57669 notiothenia
22	274	38.4	166	4	Q9H047	Q9H047 homo sapien
23	262	36.7	152	5	Q965W1	Q965W1 caenorhabdl
24	257.5	36.1	130	5	Q9VGM2	Q9VGM2 drosophila
25	254	35.6	111	13	Q90ZG6	Q90ZG6 brachydanio
26	245	34.4	86	13	Q8UWD3	Q8UWD3 anser anser
27	239.5	33.6	100	13	O57664	O57664 rhigophilla
28	235.5	33.0	137	5	O02323	O02323 caenorhabdl
29	234.5	32.9	136	5	O01814	O01814 caenorhabdl
30	234	32.8	97	11	Q9GV90	Q9GV90 mus sp. lmg
31	233.5	32.7	135	5	O01812	O01812 caenorhabdl
32	224	31.4	132	5	O61236	O61236 manduca sex
33	217.5	30.5	132	5	O26517	O26517 schistosoma
34	213.5	29.9	133	5	Q9BMK1	Q9BMK1 echinococcu
35	213.5	29.9	133	5	Q9BLX5	Q9BLX5 echinococcu
36	209.5	29.4	132	5	Q9BME8	Q9BME8 schistosoma
37	208.5	29.2	132	5	Q9UIG6	Q9UIG6 fasciola he
38	208.5	29.2	132	5	O45035	O45035 schistosoma
39	205.5	28.8	133	5	Q967X3	Q967X3 echinococcu
40	199.5	28.0	147	13	Q9PSA5	Q9PSA5 xenopus lae
41	197.5	27.7	133	5	Q9BMK2	Q9BMK2 echinococcu
42	196.5	27.6	133	5	Q9BMK3	Q9BMK3 echinococcu
43	191.5	26.9	133	5	Q8T5U9	Q8T5U9 schistosoma
44	178.5	25.0	120	5	O45036	O45036 schistosoma
45	178	25.0	98	5	Q8T5U8	Q8T5U8 schistosoma

ALIGNMENTS

RESULT 1

Q90X55 PRELIMINARY; PRT; 132 AA.
ID Q90X55 Q90X55;
AC Q90X55; Q90X56;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adipocyte fatty acid binding protein.
GN AFAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Study on chicken AFAP gene as candidate gene for fatness trait."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene in chicken."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene in chicken."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432507; AAL30744.2; -
DR EMBL; AF432506; AAL30743.1; -
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocin_cyFABP.
DR Pfam; PF00061; lipocalin; 1.

DR	PROSITE; PS00214; FARP; UNKNOWN_1.
SQ	SEQUENCE 132 AA; 14894 MW; 4F5905FAB8DA26B8 CRC64;
	Query Match 53.7%; Score 383; DB 13; Length 132; Best Local Similarity 57.6%; Pred. No. 4.5e-31; Matches 72; Conservative 19; Mismatches 34; Indels 0; Gaps 0;
Qy	9 GKWLIMESHGFEYMKELGVGLALRKMAAMAKPCDIITCDGNNTVKTSTVKTTFVFSCN 68 I::: I :: : : : : :: D b 7 GTWKLSENPFEDYMKELGVSFATRKMGAVAKPNLTISINGDVITIRSESTFKNTEISFK 66 GTWKLLS
Qy	69 LGKFFDETTADGRKTETVCTFDGCALVQHQQWDGKKESTITRKLKGKMIVECVMMNATCT 128 : : : : D b 67 LGEEFDETTADDRKTNKITLDSGTLKQVKWDGKETVIKRVRVDGNLLVECTMNNVTSK 126 LVV
Qy	129 RYVEK 133 :
D b	127 RYVER 131 :
RESULT 2	
Q8QHA8	PRELIMINARY; PRT; 132 AA.
ID	Q8QHA8
AC	Q8QHA8; 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Adipocyte fatty acid-binding protein.
OS	Anser anser (domestic goose).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX	NCBI_TaxID=8843;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=FAT;
RA	Ao J., Wang Q., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT	"Cloning and sequencing of adipocyte fatty acid-binding protein gene
RL	in goose.";
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF472610; AAL79836.1;
SQ	SEQUENCE 132 AA; 14772 MW; 5FD4817B02DA31BB CRC64;
	Query Match 52.0%; Score 371; DB 13; Length 132; Best Local Similarity 56.8%; Pred. No. 7.3e-30; Matches 71; Conservative 20; Mismatches 34; Indels 0; Gaps 0;
Qy	9 GKWLIMESHGFEYMKELGVGLALRKMAAMAKPCDIITCDGNNTVKTSTVKTTFVFSCN 68 I::: I :: : : : : :: D b 7 GTWKLSENPFEDYMKELGVSFATRKMGAVAKPNLTISINGDVITIRSESTFKNTEISFK 66 GTWKLLS
Qy	69 LGKFFDETTADGRKTETVCTFDGCALVQHQQWDGKKESTITRKLKGKMIVECVMMNATCT 128 : : : : D b 67 LGEEFDETTADDRKTNKITLDSGALKQVKGDGKETVIKRVRVDGNLLVECTMNNVTSK 126 LVV
Qy	129 RYVEK 133 :
D b	127 RYVER 131 :
RESULT 3	
Q9DAK4	PRELIMINARY; PRT; 132 AA.
ID	Q9DAK4
AC	Q9DAK4; 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	1700008G05RIK protein.
GN	1700008G05RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	- NCBI_TaxID=10090;
RN	[1]

DR		InterPro:	IPR000566;	Lipocln_cytFABP.
DR	Pfam:	PF00861;	lipocalin; 1.	
DR	PRINTS:	PR00178;	FATTYACIDBP.	
DR	PROSITE:	PS00214;	FABP; 1.	
SQ	SEQUENCE	150 AA;	9D214AB610DC54E CRC64;	
Query Match	46.78;	Score 333;	DB 11;	Length 150;
Best Local Similarity	48.8%;	Pred. No. 5.8e-26;	Mismatches 24;	Gaps 0;
Matches	61;	Conservative	Indels	0;
Qy	9	GKWLMEHSGFEEMKELGVGLALRKMAAMAKPDCIITCDGNNTIVKTSTVTKTTFVSCN	68	
Dd	7	TWKLVSSSENFDDYMKEVGVFATRVKGAGMAPNLIIISVEGDLVVIRSEFTFKNETSFVK	66	
Qy	69	LGEKFDETTADGRKETVTCTFDQDALVHQHOQGDKESTITRLKDGMIVECVMMNATCT	128	
Dd	67	LGVEFDEITPPDRKVKSITIILTDGGVLHVQKWGDGSTTIKRXXDGKLNVCECMKGVTSI	126	
Qy	129	RVYEK	133	
Dd	127	RVYXR	131	
RESULT 5				
QXSG4	ID	QXSG4 PRELIMINARY;	PRT;	113 AA.
AC	QXSG4;			
DT	01-NOV-1999 (TrEMBRel. 12,	Created)		
DT	01-NOV-1999 (TrEMBRel. 12,	Last sequence update)		
DT	01-DEC-2001 (TrEMBRel. 19,	Last annotation update)		
DE	Adipoocyte lipid-binding protein (Fragment).			
GN	Af2..			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctologus.			
NCBI_TaxID=9986;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;			
RA	Guan Y., Zhang Y., Davis L., Breyer M.D.;			
RT	"Expression of ap2 gene in transitional epithelium of rabbit bladder.";			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AF136241; AAD32209.1; "			
DR	HSP; P04117; ILID.			
DR	InterPro; IPR000463; Fatty_acid_BP.			
DR	InterPro; IPR000566; Lipocln_cytFABP.			
DR	Pfam; PF00861; lipocalin; 1.			
DR	PRINTS; PR00178; FATTYACIDBP.			
FT	NON_TER 1 1			
FT	NON_TER 113 113			
SQ	SEQUENCE	113 AA;	12536 MW;	4C1A538BC897F4F CRC64;
Query Match	46.48;	Score 331;	DB 6;	Length 113;
Best Local Similarity	55.4%;	Pred. No. 6.6e-26;	Mismatches 22;	Gaps 0;
Matches	62;	Conservative	Indels	0;
Qy	11	WRLMESGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNTIVKTSTVTKTTFVSCNLG	70	
Dd	2	KWLVSSENFFDYMEVGFGFATRVKGAGMAPNMIIISVDVIITIKSEFRWFTEISFLUG	61	
Qy	71	EKFDETADGRKETVTCTFDQDALVHQHOQGDKESTITRLKDGMIVECYM	122	
Dd	62	QEPEDEVTAADRGSKIITLDGVALVQVKWDGSKSTIKRRREGDKLVVECYM	113	
RESULT 6				
Q90W92	ID	Q90W92 PRELIMINARY;	PRT;	132 AA.
AC	Q90W92;			
DT	01-DEC-2001 (TrEMBRel. 19,	Created)		
DT	01-DEC-2001 (TrEMBRel. 19,	Last sequence update)		
DT	01-MAR-2002 (TrEMBRel. 20,	Last annotation update)		

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RESULT 9
O57691 PRELIMINARY; PRT; 134 AA.
ID AC O57691;
AC O57691;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Cryodrac antarcticus (Crocodile icefish), and
OS Chaenoccephalus acroatus (white crocodile fish).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Notothenioidae; Channichthyidae; Cryodrac.
OX NCBI_TaxID=36192; 36190;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Winnard P.,
RA Small D.J., Hatch H., Sidell B.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92443; AAC60351.1; -
DR EMBL; U92442; AAC60350.1; -
DR HSP; P10790; 1BW.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000586; Lipoclin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15138 MW; D4CBFC689147A98 CRC64;

Query Match 43.4%; Score 309.5; DB 13; Length 134;
Best Local Similarity 43.5%; Pred. No. 1.2e-23;
Matches 54; Conservative 29; Mismatches 40; Indels 1; Gaps

QY 9 GKRLMESHGFEYMKELGVGLALRKMAAKPDCIITCDGNN-ITVKTESTVKTTVFSC 67
   | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 7 GTWKMISSDNFDYMKAGVGFATRGVNTKPNLVSVDDQGFVCLKKSQSTFKTEIKF 66

QY 68 NLGEFDETTADGKKTETVCTFODGALVQHQQDGRKESTITRKLKDGKMWCEVMNATC 127
   | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 67 KLEPFETTTADDRKTKTVVTVLENGKLKQKSDGKQETNIERIEDGKLVAKKIMGDVIA 126

QY 128 TRVY 131
   | |
DB 127 VRVY 130

RESULT 10
O57665 PRELIMINARY; PRT; 134 AA.
ID AC O57665;
AC O57665;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Gobionotothen gibberifrons (Humped rockcod).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Gobionotothen.
OX NCBI_TaxID=36202;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RA MEDLINE=98129752; PubMed=9461533;
RL "Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).

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[illegible][illegible]

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RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL heart ventricle of Antarctic teleost fishes.";
DR EMBL: U92444; AAC60352.1; -.
DR HSSP: P10790; 1BWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15182 MW; D4CBCEFD50E131968 CRC64;

Query Match 42.8%; Score 305.5; DB 13; Length 134;
Best Local Similarity 43.5%; Pred. No. 3e-23;
Matches 54; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

QY 9 GKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNN-ITVKTESTVKTTFVSC 67
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 7 GTWKLMSDNEDDYKMAIGCATRGVGNRTKPNLVSVDDQGFVCLKSQSTFKTEIKF 66

QY 68 NLGEKDETTADGRKTETVCTFODGALVQHQWDGKESITIRKLKDGKMIVECVMNATC 127
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 67 KLNEPEETTADDRKTRTVTVTLNGLKLVQKQWDGKGTNIERIEDGKLVAKCIIMGDVA 126

QY 128 TRVY 131
| : : |
Db 127 VRTY 130

RESULT 14
QY18N9 PRELIMINARY; PRT; 132 AA.
AC QY18N9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Brain-type fatty-acid binding protein.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Denovan-Wright E.M., Pierce M., Wright J.M.;
RT "Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
RT binding protein and its tissue-specific expression in adult zebrafish
RT (Danio rerio).";
RL Biochim. Biophys. Acta 0:0-0(2000).
DR EMBL: AF237712; AAF79948.1; -.
DR HSSP: P10790; 1BWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;

Query Match 42.2%; Score 301; DB 13; Length 132;
Best Local Similarity 44.7%; Pred. No. 8.5e-23;
Matches 55; Conservative 24; Mismatches 44; Indels 0; Gaps 0;

QY 11 WRMLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCNLG 70
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 9 WKLVDSQNFDEYMKSLGVGFATRGVGNRTKPTIVISHGDKVVIKTLSTFKTEISFKLG 68

QY 71 EKFEDETTADGRKTETVCTFODGALVQHQWDGKESITIRKLKDGKMIVECVMNATCTRV 130
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
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Db 69 EEFEDETTADDRHVKTSTVSLGDNLVQVQRMDGKETKFFVREIKDGKVMVMTLTFFEGVOAVRT 128
QY 131 YEK 133
| : : |
Db 129 YEK 131

RESULT 15
QYUVG7 PRELIMINARY; PRT; 133 AA.
AC QYUVG7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Oocyte-type fatty-acid binding protein.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R.-Z., Denovan-Wright E.M., Wright J.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF448057; AAL40832.1; -.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 133 AA; 14882 MW; 91FB0400619A1926 CRC64;

Query Match 41.9%; Score 299; DB 13; Length 133;
Best Local Similarity 45.7%; Pred. No. 1.4e-22;
Matches 58; Conservative 24; Mismatches 45; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 7 GTWNLKESKNFDEYMKIGVGATRGVGNRTKPTIISKEGDFVTLKTVSTFKSTEINFK 66

QY 69 LGCEKDETTADGRKTETVCTFODGALVQHQWDGKESITIRKLKDGKMIVECVMNATCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 67 LGEEFEDETTADDRKVKSVITLDGKLLHVQKWDGKETTLLREVSDNNLTTLTLTGDIVST 126

QY 129 RYVEK 135
| : : |
Db 127 RHYVKA 133

Search completed: November 25, 2002, 10:24:43
Job time : 33 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:19:57 ; Search time 12 Seconds
(without alignments)
466.609 Million cell updates/sec

Title: US-09-788-074-1

Perfect score: 713

Sequence: 1 MASLKDLGKRLMESHGFE.....MIVECMNNTCTRVYKVKQ 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	100.0	135	1 FABE_MOUSE	Q05816 mus musculus
2	663	93.0	135	1 FABE_RAT	P55053 rattus norv
3	612	85.8	135	1 FABE_HUMAN	Q01469 homo sapien
4	577	80.9	135	1 FABE_BOVIN	P55052 bos taurus
5	391	54.8	131	1 MYP2_RABIT	P02691 oryctolagus
6	380	53.3	131	1 MYP2_HUMAN	P02689 homo sapien
7	375	52.6	131	1 FABA_BOVIN	P48035 bos taurus
8	373	52.3	131	1 FABA_PIG	O97788 sus scrofa
9	370	51.9	131	1 FABA_SPETR	Q99p60 spermophilu
10	369	51.8	131	1 MYP2_MOUSE	P24526 mus musculus
11	367	51.5	131	1 MYP2_BOVIN	P02690 bos taurus
12	364	51.1	132	1 FABL_GINCI	P80049 ginglymosto
13	362	50.8	131	1 FABA_HUMAN	P15090 homo sapien
14	359	50.4	131	1 FABA_MOUSE	P04117 mus musculus
15	336	47.1	132	1 FABA_RAT	P07483 rattus norv
16	335	47.0	131	1 FABA_HUMAN	P70623 rattus norv
17	334	46.8	132	1 FABH_SPETR	Q99p61 spermophilu
18	333	46.7	132	1 FABH_HUMAN	P05413 homo sapien
19	331	46.4	132	1 FABH_PIG	O02772 sus scrofa
20	320	44.9	132	1 FABH_BOVIN	P10790 bos taurus
21	320	44.9	132	1 TLBP_MOUSE	O08716 mus musculus
22	320	44.9	132	1 TLBP_RAT	P55054 rattus norv
23	318	44.6	132	1 FABH_MOUSE	P11404 mus musculus
24	308	43.2	131	1 FABB_CHICK	Q05423 gallus gall
25	302	42.4	131	1 FABB_BOVIN	Q09139 bos taurus
26	292	41.0	131	1 FABB_HUMAN	O15540 homo sapien
27	290	40.7	132	1 FABB_ONCMY	O13008 oncorhynch
28	282	39.6	131	1 FABB_MOUSE	P51880 mus musculus
29	281	39.4	131	1 FABB_RAT	P55051 rattus norv
30	273	38.3	114	1 FABL_LAMJA	P82188 lampetra ja
31	215.5	30.2	137	1 RET3_HUMAN	P05058 xenopus lae
32	213.5	29.9	133	1 FABP_ECHGR	Q02970 echinococu
33	213.5	29.9	137	1 RET4_HUMAN	P29373 homo sapien

RESULT 1

ID	FABE_MOUSE	STANDARD;	PRT;	135 AA.
AC	Q05816;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated binding protein).			
DE	fatty acid-binding protein homolog (FA-FABP) (Keratinocyte lipid-binding protein).			
GN	FABP5 OR MALL OR KLBP OR FABPE.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Keratinocytes;			
RX	MEDLINE=93352523; PubMed=8349619;			
RA	Krieg P., Feil S., Fuerstenberger G., Bowden T.G.;			
RT	"Tumor-specific overexpression of a novel keratinocyte lipid-binding protein. Identification and characterization of a cloned sequence activated during multistage carcinogenesis in mouse skin.";			
RL	J. Biol. Chem. 268:17362-17369(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RX	MEDLINE=98332726; PubMed=9666100;			
RA	Bleck B., Hohoff C., Binas B., Rustow B., Dixkens C., Hamelster H.,			
RA	Boerchers T., Spener F.;			
RT	"Cloning and chromosomal localisation of the murine epidermal-type fatty acid binding protein gene (Fabpe).";			
RL	Gene 215:123-130(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99013878; PubMed=9795232;			
RA	Hertzel A.V., Bernlohr D.A.;			
RT	"Cloning and chromosomal location of the murine Keratinocyte lipid-binding protein gene.";			
RL	Gene 221:235-243(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Stomach;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			

ALIGNMENTS

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX Strausberg R.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KERATINOCYTES AND ALSO IN
CC STRATIFIED EPITHELIA OF EPIDERMIS AND TONGUE. RELATIVELY HIGH
CC LEVELS FOUND IN ADIPOSE AND MAMMARY TISSUES AND SMALL AMOUNTS
CC FOUND IN HEART, BRAIN, LIVER, SPLEEN, MUSCLE AND LUNG.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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DR EMBL; X70100; CA449703.1; -;
DR EMBL; AJ223066; CA411069.1; -;
DR EMBL; AF061015; AAC82368.1; -;
DR EMBL; AF061014; AAC82368.1; JOINED.
DR EMBL; AK008782; BAB25890.1; -;
DR EMBL; AK011551; BAB27692.1; -;
DR EMBL; BC002008; AAH02008.1; -;
DR PIR; S36635; S36635.
DR HSSP; Q01469; 1B56.
DR MGD; MGI:101790; Fabp5.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding.
SQ SEQUENCE 135 AA; 15137 MW; 6AC8DBEB8046185 CRC64;
Query Match 100.0%; Score 713; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 2e-64;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAKPDCIITCDGNITVKTSTV 60
Db 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAKPDCIITCDGNITVKTSTV 60
QY 61 KTTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQDQDGKESTITRKLKDGKMWEC 120
Db 61 KTTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQDQDGKESTITRKLKDGKMWEC 120
QY 121 VMNNATCTRYEKVQ 135
Db 121 VMNNATCTRYEKVQ 135
RESULT 2
FABE_RAT ID FABE_RAT STANDARD; PRT; 135 AA.
AC P55053; p97757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Fatty acid-binding protein, epidermal (E-FABP) (Cutaneous fatty acid-
DE binding protein) (C-FABP) (DALI).
GN FABP5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lens;
RX MEDLINE=95331629; PubMed=7607553;
RA Wen Y., Li G.W., Chen P., Wong E., Bekhor I.;
RT "Lens epithelial cell mRNA, II. Expression of a mRNA encoding a
RT lipid-binding protein in rat lens epithelial cells.";
RL Gene 158:269-274(1995).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RX MEDLINE=94220094; PubMed=8166694;
RA Watanabe R., Fujii H., Odani S., Sakakibara J., Yamamoto A., Ito M.,
RA Ono T.;
RT "Molecular cloning of a cDNA encoding a novel fatty acid-binding
RT protein from rat skin.";
RL Biochem. Biophys. Res. Commun. 200:253-259(1994).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Nerve;
RX MEDLINE=96302634; PubMed=8723767;
RA De Leon M., Welcher A.A., Nahin R.H., Liu Y., Ruda M.A.,
RA Shooter E.M., Molina C.A.;
RT "Fatty acid binding protein is induced in neurons of the dorsal root
RT ganglia after peripheral nerve injury.";
RL J. Neurosci. Res. 44:283-292(1996).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
DR EMBL; U13253; AAA86680.1; -;
DR EMBL; S69874; AAB30574.1; -;
DR EMBL; S83247; AAB46848.1; -;
DR HSSP; Q01469; 1B56.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding.
FT CONFLICT 49 49 G -> N (IN REF. 1).
FT CONFLICT 112 112 K -> N (IN REF. 3).
SQ SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;
Query Match 93.0%; Score 663; DB 1; Length 135;
Best Local Similarity 91.9%; Pred. No. 1.9e-59;
Matches 124; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAKPDCIITCDGNITVKTSTV 60
Db 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAKPDCIITCDGNITVKTSTV 60
QY 61 KTTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQDQDGKESTITRKLKDGKMWEC 120
Db 61 KTTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQDQDGKESTITRKLKDGKMWEC 120

```
QY 121 VMNNATCTRYEKVQ 135
DB 121 VMNNAICTRYEKVQ 135

RESULT 3
FABE_HUMAN
ID FABE_HUMAN STANDARD; PRT; 135 AA.
AC Q01469;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP).
GN FABP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Keratinocytes;
RX MEDLINE=92381332; PubMed=1512466;
RA Madsen P.S., Rasmussen H.H., Jeffers H., Honore B., Celis J.E.;
RT "Molecular cloning and expression of a novel keratinocyte protein
RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
RT highly up-regulated in psoriatic skin and that shares similarity to
RT fatty acid-binding proteins."
RL J. Invest. Dermatol. 99:299-305(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
RN [4]
RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
RX MEDLINE=94379963; PubMed=8092987;
RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
RA Hellman U., Saurat J.-H.;
RT "Purification and characterization of the human epidermal fatty acid-
RT binding protein: localization during epidermal cell differentiation
RT in vivo and in vitro."
RL Biochem. J. 302:363-371(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=99425110; PubMed=10493790;
RA Hohoff C., Borchers T., Rustow B., Spener F., van Tilbeurgh H.;
RT "Expression, purification and crystal structure determination of
RT recombinant human epidermal-type fatty acid-binding protein."
RL Biochemistry 38:12229-12239(1999).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING
CC DOUBLE BONDS REDUCES THE AFFINITY. MAY BE INVOLVED IN KERATINOCYTE
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
CC SKIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC
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CC
DR EMBL; M94856; AAA58467.1; -.
DR EMBL; BC019385; AAH19385.1; -.
DR PDB; 1B56; 05-OCT-99.
DR Aarhus/Ghent-2DPAGE; 3007; IEF.
DR Genew; HGNC:3560; FABP5.
DR MIM; 605168; -.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PRO0178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; 3D-structure.
SQ SEQUENCE 135 AA; 15164 MW; 77D38F8806143D63 CRC64;

Query Match 85.8%; Score 612; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 2.4e-54;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 MASLKDECKWRLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTV 60
DB 1 MATVQLEGRLVDSKGFDEYNKELGVGLALRKMAAMAKPDCIITCDGNLTIKTSTL 60
QY 61 KTVFSCNLGERKFDFTADGRKTETCTTQDQALVQHQQWQDGKESITTRKLDKRMIVEC 120
DB 61 KITQFSCTLGKFEFTADGRKTQTVCFNFDGALVQHQQWQDGKESITTRKLDKGLVVEC 120
QY 121 VMNNATCTRYEKVQ 135
DB 121 VMNNTCTRYEKVE 135

RESULT 4
FABE_BOVIN
ID FABE_BOVIN STANDARD; PRT; 135 AA.
AC P55052; O62808;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Differentiation-
DE associated lipid binding protein LP2).
GN FABP5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129.
RC TISSUE=Lens;
RX MEDLINE=97103094; PubMed=8947466;
RA Jaworski C., Wistow G.;
RT "LP2, a differentiation-associated lipid-binding protein expressed in
RT bovine lens."
RL Biochem. J. 320:49-54(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=98198033; PubMed=9521644;
RA Kingma P.B., Bok D., Ong D.E.;
RT "Bovine epidermal fatty acid-binding protein: determination of ligand
RT specificity and cellular localization in retina and testis."
RL Biochemistry 37:3250-3257(1998).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN
CC THE UPTAKE AND TRANSPORT OF FATTY ACIDS ESSENTIAL FOR THE
CC NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL
CC TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND RETINA (FOUND IN THE
```

CC MUELLER CELLS), MODERATELY ABUNDANT IN HEART AND TESTIS (FOUND IN
CC THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
CC EMBL: U55188; AAC14297.1; ..
CC EMBL: AF059507; AAC14711.1; ..
CC HSSP: Q01469; 1B56.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam: PF00061; lipocalin; 1.
CC PRINTS: PR00178; FATTYACIDBP.
CC PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT MOD_RES 22 22 PHOSPHORYLATION (BY TYR-KINASES)
FT CONFLICT 52 52 L -> P (IN REF. 1).
FT SEQUENCE 135 AA; 15074 MW; 439B86AF88A34E2A CRC64;
Query Match 80.9%; Score 577; DB 1; Length 135;
Best Local Similarity 76.3%; Pred. No. 7.6e-51;
Matches 103; Conservative 20; Mismatches 12; Indels 0; Gaps 0;
QY 1 MASLKDEGKRWLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60
Db 1 MATVQQLVGRWRLVESGDFEYKVGCVGNALRKVGAMAKPDCIITSDGNLSIKTESTL 60
QY 61 KTTVFSCNKEKEDETTADGRKRTVCTFODGALVQHQWDGKESITTRKLKDKGMIVEC 120
Db 61 KTTQFSCKLGEFEETADGRKRTVCTVCTFODGALVQHQWDGKESITTRKLKDKGMIVEC 120
QY 121 VMNNATCTRYVEKVO 135
Db 121 VMNNVCTRYVEKVE 135
RESULT 5
MYP2_RABIT STANDARD; PRT; 131 AA.
AC P02691; 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228063; PubMed=2453513;
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT "Characterization of a cloned cDNA encoding rabbit myelin P2
RT protein.";
RL J. Biol. Chem. 263:8332-8337(1988).
RN [2]
RP SEQUENCE OF 1-55.
RX MEDLINE=80094496; PubMed=7356651;
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin.";
RL J. Biol. Chem. 255:1058-1063(1980).
RN [3]
RP SEQUENCE OF 55-131.

RX MEDLINE=82098098; PubMed=6172423;
RA Ishaque A., Hofmann T., Eylar E.H.;
RT "The complete amino acid sequence of the rabbit P2 protein.";
RL J. Biol. Chem. 257:592-595(1982).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03744; AAA31451.1; ..
CC PIR: A03145; MPRB2.
CC PIR: A28081; A28081.
CC HSSP: P02690; 1PMP.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam: PF00061; lipocalin; 1.
CC PRINTS: PR00178; FATTYACIDBP.
CC PROSITE: PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 72 72 E -> Q (IN REF. 3).
FT CONFLICT 83 83 I -> T (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 3).
SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;
Query Match 54.8%; Score 391; DB 1; Length 131;
Best Local Similarity 57.9%; Pred. No. 2.8e-32;
Matches 73; Conservative 22; Mismatches 31; Indels 0; Gaps 0;
QY 9 GKWRMLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVTFSCN 68
Db 6 GTWKLVSSFNDDYMKALGVGLATRLKGLAKPNVLSKKGDIITRTTESTFKNTEISPK 65
QY 69 LCEKFDETTADGRKRTVCTFODGALVQHQWDGKESITTRKLKDKGMIVECVNNATCT 128
Db 66 LGQEFEEETADNRKTSIITLGERGALNQVQKDGKETTIRKLKLVGKMVVECKMGVVC 125
QY 129 RYVEKV 134
Db 126 RYVEKV 131
RESULT 6
MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689; 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;
RT "Isolation and sequence determination of cDNA encoding P2 protein of

```
RT human peripheral myelin.";
RL Biochem. Biophys. Res. Commun. 181:204-207(1991).
RN [2]
RP SEQUENCE.
RX MEDLINE=83058785; PubMed=6183401;
RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
RT "The complete amino acid sequence of human P2 protein.";
RL J. Neurochem. 39:1759-1762(1982).
RN [3]
RP SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=95054012; PubMed=7525873;
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
RA Tennekoon G.;
RT "Partial structure and mapping of the human myelin P2 protein gene.";
RL J. Neurochem. 63:2010-2013(1994).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
DR EMBL; D16181; BAA03726.1; -.
DR EMBL; D16179; BAA03726.1; JOINED.
DR EMBL; D16180; BAA03726.1; JOINED.
DR EMBL; X62167; CAA44096.1; -.
DR EMBL; S73470; AAB32592.1; -.
DR EMBL; S73468; AAB32592.2; JOINED.
DR EMBL; S73469; AAB32592.2; JOINED.
DR PIR; A03143; MPH02.
DR PIR; J00977; J00977.
DR HSP; P02690; 1PWP.
DR Genew; HGNC:9117; PMP2.
DR MIM; 170715; -.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLTATION.
FT SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;
Query Match 53.3%; Score 380; DB 1; Length 131;
Best Local Similarity 56.3%; Pred. No. 3.5e-31;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRKMMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKALGVGLATRLKGLNLAFTVIISKKGDIITRTSTFKNTSEISFK 65
QY 69 LGEKFDFTADGRKTTVTCTFDGALVGHQWDGKSTITRKLKDGKMKIVECVNNATCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGOEFDEFTADNRKTSIVTLQGSLSNVQVRWDGKSTITRKLKDLVNGKVMACKMGVCT 125
QY 129 RYVEKV 134
Db 126 RYVEKV 131
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RESULT 7
FABA_BOVIN
ID FABA_BOVIN STANDARD; PRT; 131 AA.
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
GN FAPB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartetzko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers T., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
DR EMBL; X89244; CAA61532.1; -.
DR HSP; P04117; 1LID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 19 19 PHOSPHORYLTATION (BY TYR-KINASES)
FT SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;
Query Match 52.6%; Score 375; DB 1; Length 131;
Best Local Similarity 55.2%; Pred. No. 1.1e-30;
Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRKMMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKELGVGFATRVAGNAKPTLIISLNGGVVTVIKSETFKNTSEISFK 65
QY 69 LGEKFDFTADGRKTTVTCTFDGALVGHQWDGKSTITRKLKDGKMKIVECVNNATCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGOEFDEFTDPRKVKSIYNLDEGALVQVQNDGKSTITRKLKDLVNGKVMACKMGVCT 125
QY 129 RYVEKV 133
Db 126 RYVEKV 130
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RESULT 8
FABA_PIG
ID FABA_PIG STANDARD; PRT; 131 AA.
AC O97788;
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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (AP2).
GN FABP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Duroc; TISSUE=Liver;
RX MEDLINE=99099248; PubMed=980671;
RA Gerbens F.N.A., Jansen A., van Erp A.J.M., Harders F.,
RA Meuwissen T.H.E., Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
RT "The adipocyte fatty acid-binding protein locus: characterization and
RT association with intramuscular fat content in pigs.";
RL Mamm. Genome 9:1022-1026(1998).
RN [2]
RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
RC TISSUE=Fat;
RX MEDLINE=90241143; PubMed=2334399;
RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
RT "The purification and characterization of a fatty acid binding protein
RT specific to pig (Sus domesticus) adipose tissue.";
RL Biochem. J. 267:373-378(1990).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT
CC ACCRETION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: ADIPOSE TISSUE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
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CC -----
DR EMBL; Y16039; CAA75995.1; -.
DR EMBL; AJ416020; CAC95166.1; -.
DR HSP; P04117; 1L1D.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14545 MW; 656CB0CA08CDA4B2 CRC64;
Query Match 52.3%; Score 373; DB 1; Length 131;
Best Local Similarity 53.6%; Pred. No. 1.8e-30;
Matches 67; Conservative 25; Mismatches 33; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRRKMAAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
DB 6 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNLIITVNGDMITIRSESTFKNTEIAFK 65
QY 69 LGKEFDETTADGKRTVCTVCTFDGALVQHQQDQKGKSTITRKLKDGKMTVECVMMNATCT 128
DB 66 LGQEFDEVATDDKRVKSTITLGGALVQVQKQKGTITINRKRVDKLVVEICIMKGVAT 125
QY 129 RYVEK 133
DB 126 RYVER 130
RESULT 10
MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
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DB 126 RYVER 130
RESULT 9
FABA_SPEPR
ID FABA_SPEPR STANDARD; PRT; 131 AA.
AC Q99B60;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Spemophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Spemophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittel D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding
RT proteins in hibernating ground squirrels.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBB databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
DR EMBL; AF327855; AAK08084.1; -.
DR HSP; P04117; 1L1D.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14634 MW; FCEE7B092A2AF708 CRC64;
Query Match 51.9%; Score 370; DB 1; Length 131;
Best Local Similarity 54.4%; Pred. No. 3.5e-30;
Matches 68; Conservative 24; Mismatches 33; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRRKMAAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
DB 6 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNLIITVNGDMITIRSESTFKNTEISFK 65
QY 69 LGKEFDETTADGKRTVCTVCTFDGALVQHQQDQKGKSTITRKLKDGKMTVECVMMNATCT 128
DB 66 LGQEFDEVATDDKRVKSTITLGGALVQVQKQKGTITIKRKRDDKLVVEICIMKGVAT 125
QY 129 RYVEK 133
DB 126 RYVER 130
RESULT 10
MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
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DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSP; P02690; 1PMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 51.8%; Score 369; DB 1; Length 131;
Best Local Similarity 54.0%; Pred. No. 4.5e-30;
Matches 68; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKAKSIVTLERGLSKQVQKWDGKETAIRRTLLDGRMVVCEIMKGVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 11
MYP2_BOVIN
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSP; P02690; 1PMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 51.8%; Score 369; DB 1; Length 131;
Best Local Similarity 54.0%; Pred. No. 4.5e-30;
Matches 68; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKAKSIVTLERGLSKQVQKWDGKETAIRRTLLDGRMVVCEIMKGVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 11
MYP2_BOVIN
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80225120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine
RT peripheral nerve myelin.";
RL FEBS Lett. 115:27-30(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=89005045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBO J. 7:1597-1604(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=93253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic
RT transport proteins. Refinement of P2 myelin protein and the structure
RT determination and refinement of cellular retinol-binding protein in
RT complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC PIR; A03144; MPB02.
CC PDB; 1PMP; 26-JAN-95.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
FT MOD_RES 1 1 ACETYLATION.
FT DISULFD 117 124
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 51.5%; Score 367; DB 1; Length 131;
Best Local Similarity 55.6%; Pred. No. 7.1e-30;
Matches 70; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKKTSTVTLARGSLNQVQKWNGETTITRKLVDGKMWVECKMKDVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 12
FABL_GINCI
ID FABL_GINCI STANDARD; PRT; 132 AA.
AC P80049;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Fatty acid-binding protein, liver (L-FABP).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Ginglymostomatidae; Ginglymostoma.
OX NCBI_TaxID=7801;
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RN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=92137215; PubMed=1735421;
RA Medzihradsky K.F., Gibson B.W., Kaur S., Yu Z., Medzihradsky D.,
RA Burlingame A.L., Bass N.M.;
RT "The primary structure of fatty-acid-binding protein from nurse shark
RT liver. Structural and evolutionary relationship to the mammalian
RT fatty-acid-binding protein family."
RL Eur. J. Biochem. 203:327-339(1992).
CC !- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC !- SUBCELLULAR LOCATION: Cytoplasmic.
CC !- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR PIR: S20297; S20297.
DR HSSP: P05413; LHWT.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PRO0178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Acetylation; Phosphorylation.
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT MOD_RES 19 19 (POTENTIAL).
FT SEQUENCE 132 AA; 15079 MW; 2AFDEA2C0BE2095F CRC64;

Query Match 51.1%; Score 364; DB 1; Length 132;
Best Local Similarity 53.5%; Pred. No. 1.4e-29;
Matches 68; Conservative 21; Mismatches 38; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEYMKELGVGLALRMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
DB 6 GSKWLKSHNFDEYMKNLDSLAQRVATVPKTIISLDGVDITIKTESTFKSTNIQFK 65
QY 69 LGKEFDETTADGKRTVCTFODGALVQHQWDGKESTITRKLKDGKMTVECMNNATCT 128
DB 66 LAEEFDETTADNRNRTTKTVKLENGKLVQTORWDGKRTTLVRELQDGKLLITCTMGDVVCT 125
QY 129 RYVEKVQ 135
DB 126 RYVREQ 132

RESULT 13
FABA_HUMAN STANDARD; PRT; 131 AA.
AC P15090;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105397; PubMed=2481498;
RA Baxa C.A., Sha R.S., Buel M.K., Smith A.J., Matarese V.,
RA Chinander L.L., Boundy K.L., Bernlohr D.A.;
RT "Human adipocyte lipid-binding protein: purification of the protein
RT and cloning of its complementary DNA."
RL Biochemistry 28:8683-8690(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG

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CC CHAIN FATTY ACID AND RETINOIC ACID.
CC !- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC !- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
DR EMBL: J02874; AAA51689.1; -.
DR EMBL: BC003672; AAH03672.1; -.
DR PIR: A33363; A33363.
DR HSSP: P04117; LLID.
DR Genew; HGNC:3559; FABP4.
DR MIM: 600434; -.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PRO0178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT MOD_RES 19 19 (BY SIMILARITY).
FT SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;

Query Match 50.8%; Score 362; DB 1; Length 131;
Best Local Similarity 54.4%; Pred. No. 2.2e-29;
Matches 68; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEYMKELGVGLALRMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
DB 6 GTWLKSHNFDEYMKNLDSLAQRVATVPKTIISLDGVDITIKTESTFKSTNIQFK 65
QY 69 LGKEFDETTADGKRTVCTFODGALVQHQWDGKESTITRKLKDGKMTVECMNNATCT 128
DB 66 LGQEFDEVTDADRKVKSTITLDGGVLVHVQKWDGKSTTIIRKREDDKLVEECVMKGVST 125
QY 129 RYVEK 133
DB 126 RYVER 130

RESULT 14
FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (P2 adipocyte protein) (Myelin P2 protein
DE homolog) (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RT identification of an mRNA encoding a homologue of myelin P2
RT protein."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233319; PubMed=3520554;

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FT CONFLICT 69 69 E -> Q (IN REF. 5).
FT CONFLICT 70 70 F -> D (IN REF. 3).
FT CONFLICT 115 115 L -> LL (IN REF. 6).
SQ SEQUENCE 132 AA; 14643 MW; 31B4C6GA8BFB45BE CRC64;

Query Match 47.1%; Score 336; DB 1; Length 132;
Best Local Similarity 51.2%; Pred. No. 8.9e-27;
Matches 64; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 9 GKWRLMESHGFEEYMKELGVLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
Db 6 GTWKLVDSKNFDDYMKSLGSGVGFATRQVASMTKPTTIIKNGDTITIKTHSTPKNTEISFQ 65
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
QY 69 LGEKFDETTADGRKTTVCTFQDQALVQHQQWDGKESTITRKLKDGKMIVECVMMNATCT 128
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
Db 66 LGVFDEVTADDRKVKSVVTLDDGKLVHVQKWDGQETTLTRELSDGKLILTLTHGNVST 125
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
QY 129 RVYEK 133
   |:::|
Db 126 RYEK 130
   |:::|

Search completed: November 25, 2002, 10:24:05
Job time : 13 secs
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:34:08 ; Search time 30 Seconds

(without alignments)
927.212 Million cell updates/sec

Title: US-09-788-074-3

Perfect score: 711

Sequence: 1 MATVQQLGGRRLVDSKGF.....LVVECMNVNVTCTRIYKVE 135

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mmc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	52.6	132	13 Q90X55	Q90X55 gallus gall
2	369	51.9	132	11 Q9DAK4	Q9DAK4 mus musculus
3	359	50.5	132	13 Q8QHA8	Q8QHA8 anser anser
4	334	47.0	150	11 Q9R290	Q9R290 rattus norv
5	333	46.8	132	13 Q90W92	Q90W92 fundulus he
6	331.5	46.6	134	13 Q57665	Q57665 gobionototh
7	331.5	46.6	134	13 Q57691	Q57691 cryodraco a
8	330	46.4	132	11 Q9DAL2	Q9DAL2 mus musculus
9	329.5	46.3	134	13 Q57666	Q57666 parahealic
10	329	46.3	113	6 Q9XSG4	Q9XSG4 oryctolagus
11	327.5	46.1	134	13 Q57663	Q57663 nototenia
12	326	45.9	135	13 Q91896	Q91896 anguilla ja
13	320	45.0	125	6 Q9XS15	Q9XS15 equus cabal
14	313	44.0	132	13 Q918N9	Q918N9 brachydanio
15	304	42.8	133	13 Q8UVG7	Q8UVG7 brachydanio
16	296	41.6	133	13 Q57668	Q57668 cryodraco a

17	295	41.5	133	13	Q57667	O57667.chaenocepha
18	295	41.5	133	13	Q57670	O57670 gobionototh
19	295	41.5	136	5	Q8WR15	Q8WR15 metapenaeus
20	294	41.4	133	13	Q57669	Q57669 nototenia
21	281	39.5	166	4	Q9H047	Q9H047 homo sapien
22	277	39.0	99	6	O97675	O97675 sus scrofa
23	256	36.0	111	13	Q90ZG6	Q90ZG6 brachydanio
24	253.5	35.7	130	5	O9VGM2	O9VGM2 drosophila
25	253	35.6	152	5	Q965W1	Q965W1 caenorhabdi
26	244.5	34.4	100	13	Q57664	Q57664 rhigophila
27	234.5	33.0	135	5	O01812	O01812 caenorhabdi
28	231.5	32.6	137	5	O02323	O02323 caenorhabdi
29	230	32.3	86	13	Q8UWD3	Q8UWD3 anser anser
30	224.5	31.6	136	5	O01814	O01814 caenorhabdi
31	222.5	31.3	133	5	Q9BMK1	Q9BMK1 echinococcu
32	222.5	31.3	133	5	Q9BLY5	Q9BLY5 echinococcu
33	222	31.2	97	11	Q9QV90	Q9QV90 mus sp. lmg
34	215.5	30.3	133	5	Q967X3	Q967X3 echinococcu
35	211.5	29.7	132	5	O61236	O61236 manduca sex
36	209.5	29.5	132	5	Q9U1G6	Q9U1G6 fasciola he
37	209.5	29.5	133	5	Q9BMK2	Q9BMK2 echinococcu
38	208.5	29.3	133	5	Q9BMK3	Q9BMK3 echinococcu
39	200.5	28.2	132	5	Q26517	Q26517 schistosoma
40	194.5	27.4	147	13	Q9PSA5	Q9PSA5 xenopus lae
41	192.5	27.1	132	5	Q9BME8	Q9BME8 schistosoma
42	191.5	26.9	132	5	O45035	O45035 schistosoma
43	184.5	25.9	133	5	Q8T5U9	Q8T5U9 schistosoma
44	171	24.1	128	13	Q919A9	Q919A9 lygodactylu
45	169	23.8	98	5	Q8T5U8	Q8T5U8 schistosoma

ALIGNMENTS

RESULT 1

Q90X55 PRELIMINARY; PRT: 132 AA.

ID Q90X55; Q90X56;

AC Q90X55; Q90X56;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Adipocyte fatty acid binding protein.

GN AFABP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;

RT "Study on chicken AFABP gene as candidate gene for fatness trait.;"

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Wang Q., Li N., Li H.;

RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

in chicken.;"

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Wang Q., Li N., Li H.;

RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

in chicken.;"

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AF432507; AAL30744.2; -

EMBL; AF432506; AAL30743.1; -

DR InterPro: IPR000463; Fatty_acid_BP.

DR InterPro: IPR000566; Lipocalin_cytFABP.

DR Pfam: PF00061; lipocalin; 1.

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DR PROSITE; PS00214; FAPB; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14894 MW; 4F5905FAB8DA268B CRC64;

Query Match
Best Local Similarity 52.6%; Score 374; DB 13; Length 132;
Matches 70; Conservative 22; Mismatches 36; Indels 0; Gaps 0;

QY 6 QLEGRWRLVDSKGFDEYMKELGVIALRKMAGAKPDCIITCDGKNLTIKTESTLKTQF 65
Db 4 QFVGTKLLSSENFEDYMKELGVGFATRKMGAVAKPNLTISINGDVITIRSESTFKNTEI 63

QY 66 SCTLGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKGESTTRKLDKGLVVECVNNV 125
Db 64 SFKLGEFEEDTADRRKTNVITLDSCTLQVQKQWBGDKETVIRKRVVDGNLLVECTMNV 123

QY 126 TCTRIYEK 133
Db 124 TSKRVYER 131

RESULT 2
Q9DAK4
ID Q9DAK4 PRELIMINARY; PRT; 132 AA.
AC Q9DAK4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 1700008G05RIK protein.
GN 1700008G05RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant F.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK05765; BAB24227.1; -.
DR HSSP; P02690; 1PMP.
DR MGD; MGI:1922747; 1700008G05RIK.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 132 AA; 14758 MW; 7A20C53780845F61 CRC64;

Query Match
Best Local Similarity 51.9%; Score 369; DB 11; Length 132;
Matches 71; Conservative 22; Mismatches 38; Indels 0; Gaps 0;

QY 4 VOQLEGRWRLVDSKGFDEYMKELGVIALRKMAGAKPDCIITCDGKNLTIKTESTLKT 63
Db 2 VOQLQGTWRSVSCDNPENYMKELGVGRSKLGLCLAKPTVTISTDGLTIKTSIFRKN 61

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QY 64 QFCTLGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKGESTTRKLDKGLVVECVN 123
Db 62 EIFKLGEEFEETTPSGRKSSTVILDNDSLVQVQDMDGREATICRLVDGKMWVESAVN 121

QY 124 NVTCTRIYEKV 134
Db 122 NVTCTRTYQRV 132

RESULT 3
Q8QHA8
ID Q8QHA8 PRELIMINARY; PRT; 132 AA.
AC Q8QHA8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Adipocyte fatty acid-binding protein.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Ao J., Wang Q., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid-binding protein gene
RT in goose.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF472610; AAL79836.1; -.
SQ SEQUENCE 132 AA; 14772 MW; 5FD4817B02DA31BB CRC64;

Query Match
Best Local Similarity 50.5%; Score 359; DB 13; Length 132;
Matches 68; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVIALRKMAGAKPDCIITCDGKNLTIKTESTLKTQFSC 68
Db 7 GTWKLSSSENFEDYMKELGVGFATRKMGAVAKPNLTISINGDVITIRSESTFKNTEIS 66

QY 69 LGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKGESTTRKLDKGLVVECVNNVTCT 128
Db 67 LGEEFEEDTADRRKTNVITLDSGLKQVQKQWBGDKETVIRKRVVDGNLLVECTMNVTSK 126

QY 129 RIVEK 133
Db 127 RYVER 131

RESULT 4
Q9R290
ID Q9R290 PRELIMINARY; PRT; 150 AA.
AC Q9R290;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Adipocyte lipid-binding protein.
GN ALBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=ADIPOSE TISSUE;
RX MEDLINE=99254074; PubMed=10318917;
RA Shen W.-J., Sridhar K., Bernalhr D.A., Kraemer F.B.;
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-
RT binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
DR EMBL; AF144756; AAD37371.1; -.
DR HSSP; P04117; LLID.
DR InterPro; IPR000463; Fatty_acid_BP.

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DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
SQ SEQUENCE 134 AA; 15138 MW; D4CBCFC689147A98 CRC64;

Query Match 46.6%; Score 331.5; DB 13; Length 134;
Best Local Similarity 46.5%; Pred. No. 2.4e-26;
Matches 60; Conservative 28; Mismatches 40; Indels 1; Gaps 1;

QY 4 VOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGMAMKAPDCIITCDGKN-ITIKTESTLKT 62
DQ 2 VERKFGVTWKMISSDNFDDYMKALGVGFATRVGNRTKPNLVSVDDQGFVCLKSQSTFKT 61
QY 63 TQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVN 122
DQ 62 TEIKFKLNEPFEETADDRKTQTVVTVLENGKLVQKQSDGKGTNIETIEDGKLVAKCIM 121
QY 123 NNVTCTRIY 131
DQ 122 GDVIAVRTY 130
QY 123 NNVTCTRIY 131
DQ 122 GDVIAVRTY 130

RESULT 8
Q9DAL2 PRELIMINARY; PRT; 132 AA.
AC Q9DAL2
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 1700007P10RIK protein.
GN 1700007P10RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005745; BAB24218.1; -.
DR HSSP; P02690; 1PWP.
DR MGD; MGI:1917230; 1700007P10RIK.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
SQ SEQUENCE 132 AA; 15017 MW; D52B2279F0A7E272 CRC64;

Query Match 46.4%; Score 330; DB 11; Length 132;
Best Local Similarity 45.8%; Pred. No. 3.3e-26;
Matches 60; Conservative 30; Mismatches 41; Indels 0; Gaps 0;

QY 4 VOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGMAMKAPDCIITCDGKN-ITIKTESTLKT 63

Db 2 IEFFLGTWKLISSENFENYVRELGVCEPRKVKACLKPSVSI5FNGERMIDQAGSACRNT 61
QY 64 QFSCITLGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVN 123
Db 62 EISFKLGEFEETADNRKVKSLITFEGGSNIQVQKWLQKQTTIKRKIVDGRKVVVECTMN 121
QY 124 NVTCCTRIYKV 134
Db 122 NVVSTRIYERV 132
RESULT 9
O57666 PRELIMINARY; PRT; 134 AA.
AC O57666
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Paracheenichthys charcoti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Bathyracnidae; Paracheenichthys.
OX NCBI_TaxID=36187;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL Biochem J 330:375-382(1998).
DR EMBL; U92447; AAC60355.1; -.
DR HSSP; P10790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
SQ SEQUENCE 134 AA; 15161 MW; D4CBCFC689121AFE CRC64;

Query Match 46.3%; Score 329.5; DB 13; Length 134;
Best Local Similarity 46.5%; Pred. No. 3.8e-26;
Matches 60; Conservative 28; Mismatches 40; Indels 1; Gaps 1;

QY 4 VOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGMAMKAPDCIITCDGKN-ITIKTESTLKT 62
Db 2 VERKFGVTWKMISSDNFDDYMKALGVGFATRVGNRTKPNLVSVDDQGFVCLKSQSTFKT 61
QY 63 TQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVN 122
Db 62 TEIKFKLNEPFEETADDRKTQTVVTVLENGKLVQKQSDGKGTNIETIEDGKLVAKCIM 121
QY 123 NNVTCTRIY 131
Db 122 GDVIAVRTY 130
RESULT 10
Q9XSG4 PRELIMINARY; PRT; 113 AA.
AC Q9XSG4
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Adipocyte lipid-binding protein (fragment).
GN AP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.


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OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
   bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136241; AAD32209.1; -.
DR HSSP: P04117; ILID.
DR InterPro: IPR000463; Fatty_acid_BP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 46.3%; Score 329; DB 6; Length 113;
Best Local Similarity 56.2%; Pred. No. 3.5e-26;
Matches 63; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 11 WRLVDSKGFDEYMKELGVGIALRMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCITLG 70
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 WKLVSENFDYMKVEGVGFATRKRVAGMAPNMIISVNGDVITIKSESTFKNTEISPKLG 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 71 EKFEETADGRKTQTYCNFTDQALVQHOEWGDKGKSTITRKLDGKLVEECVM 122
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 QEPDEVTADDRKSKSIITLDGALVQVQKWGSKSTTIKRRKREGDKLVEECVM 113
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

* RESULT 11
O57663 PRELIMINARY; PRT; 134 AA.
AC O57663;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
.DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-Isoform.
GN H6-FABP.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidei; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
   heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL: U92444; AAC60352.1; -.
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15182 MW; D4CBDFD50E131968 CRC64;

Query Match 46.1%; Score 327.5; DB 13; Length 134;
Best Local Similarity 46.5%; Pred. No. 6.1e-26;
Matches 60; Conservative 28; Mismatches 40; Indels 1; Gaps 1;

QY 4 VOQLEGRWRLVDSKGFDEYMKELGVGIALRMGAMAKPDCIITCDGKNLTIKTESTPLKT 62
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 VERFVGTWKNISSDNFDYMKAGVGFATQVGNRTKPNLVSVDDGQFFVCLKSQSTFKT 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 TQFSCITLGEKFETTADGRKTQTYCNFTDQALVQHOEWGDKGKSTITRKLDGKLVEECVM 122
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DB 62 TEIKFKLNEPFETTADDRKTRTVVTLNGLKLVQKQWCGKETNIERIEDGKLVAKCIM 121
QY 123 NNVTCTRIY 131
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 GDVIAVRTY 130
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q91896 PRELIMINARY; PRT; 135 AA.
AC Q91896;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heart fatty acid binding protein.
GN H-FABP.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Teratani T., Nozawa R.;
RT "cDNA for heart fatty acid binding protein, from intron-1
   to exon-4.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Teratani T., Nozawa R.;
RT "The eel heart fatty acid binding protein.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039666; BAA92355.2; -.
DR EMBL: AB039665; BAA92355.2; JOINED.
DR EMBL: AB038695; BAA92241.3; -.
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 135 AA; 15268 MW; 0FLCC8607D38F70B CRC64;

Query Match 45.9%; Score 326; DB 13; Length 135;
Best Local Similarity 47.4%; Pred. No. 8.8e-26;
Matches 64; Conservative 19; Mismatches 52; Indels 0; Gaps 0;

QY 1 MATVQQLGRWRLVDSKGFDEYMKELGVGIALRMGAMAKPDCIITCDGKNLTIKTESTL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MVIMEPFLGTWHLKTSNFDYMKELGVGIFATRKIGNTTKPTLIIAADGDKFQVKTSLL 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 KTTQFSCITLGEKFETTADGRKTQTYCNFTDQALVQHOEWGDKGKSTITRKLDGKLVEEC 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 KSTEINFKLGEFDETTADDRKRVKSVVVKLEDGKLVHLQKWDSKETSLVRAVDGKNLTTL 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 VMNVTCTRIYKVE 135
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 TFGNVVSTRHYRAE 135
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q9XS15 PRELIMINARY; PRT; 125 AA.
AC Q9XS15;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Heart-type fatty acid-binding protein (Fragment).
GN FABP3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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Db      69 EEFDETTADDRHVKSTVSLQEDNLVQVRWDGRTKFKVREIKDGKMVMTLTFEGVAVRT 128
QY      131 YEK 133
       |||
Db      129 YEK 131
       |||

RESULT 15
QBUNVG7 PRELIMINARY; PRT; 133 AA.
AC QBUNVG7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oocyte-type fatty-acid binding protein.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R.-Z., Denovan-Wright E.M., Wright J.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RS EMBL; AF448057; AAL40832.1; -.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin_1
DR PRINTS; PR00178; FATYACIDBP.
DR PROSITE; PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 133 AA; 14882 MW; 91FB0400619A1926 CRC64;

Query Match 42.8%; Score 304; DB 13; Length 133;
Best Local Similarity 45.7%; Pred. No. 1.6e-23;
Matches 58; Conservative 24; Mismatches 45; Indels 0; Gaps 0

QY      9 GRMLVDSKGFEYMKELGVGIARLRKMANAKPDCTITCDGNLTIKTTESTLKTTOFSCT 68
       ||| ||||| ||||| ||| ||| ||| ||| ||| ||| : | || ||| :
Db      7 GTNWLRESKNDEYMGIGVGFATRQVANMTKPTTIISREGDVFTLKTVSTPKSTEINFK 66
       ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| : | || ||| :

QY      69 LGKEFFETTDAGRKQTVCVNFTDGAIVHQEWGDKGSTTRKLKDGLVVCECVNNVTCT 128
       ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| : | || ||| :
Db      67 LGEFDFTTADDRKRVSVITLDGGKKLLHVQWGDGKETTLLEKYSDNNLTLTTLGLDIVST 126
       ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| : | || ||| :

QY      129 RIVEKVE 135
       ||| |||
Db      127 RHVYKAE 133
       ||| |||

Search completed: November 25, 2002, 10:36:31
Job time : 30 secs

```

Search completed: November 25, 2002, 10:36:31
Job time : 30 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:31:53 ; Search time 12 Seconds
(without alignments)
466.609 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVQQLGGRWRLVDSKGF.....LVVECVNNVTCTRIYKVE 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	135	1	FABE_HUMAN
2	658	92.5	135	1	FABE_BOVIN
3	612	86.1	135	1	FABE_MOUSE
4	611	85.9	135	1	FABE_RAT
5	402	56.5	131	1	MYP2_RABIT
6	387	54.4	131	1	MYP2_HUMAN
7	382	53.7	131	1	FABA_BOVIN
8	382	53.7	131	1	MYP2_BOVIN
9	376	52.9	131	1	FABA_PIG
10	373	52.5	131	1	MYP2_MOUSE
11	371	52.2	131	1	FABA_SPETR
12	366	51.5	131	1	FABA_HUMAN
13	360	50.6	131	1	FABA_MOUSE
14	344	48.4	132	1	FABH_RAT
15	344	48.4	132	1	FABL_GINCI
16	343	48.2	132	1	FABH_SPETR
17	337	47.4	131	1	FABA_HUMAN
18	336	47.3	131	1	FABA_RAT
19	333	46.8	132	1	FABH_PIG
20	331	46.6	132	1	FABH_BOVIN
21	326	45.9	132	1	FABH_MOUSE
22	319	44.9	132	1	TLBP_RAT
23	318	44.7	132	1	TLBP_MOUSE
24	310	43.6	132	1	FABH_ONCMY
25	308	43.3	131	1	FABH_BOVIN
26	307	43.2	131	1	FABH_CHICK
27	304	42.8	131	1	FABH_MOUSE
28	303	42.6	131	1	FABH_HUMAN
29	303	42.6	131	1	FABH_RAT
30	286	40.2	114	1	FABL_LAMJA
31	222.5	31.3	133	1	FABP_ECHGR
32	214.5	30.2	137	1	RET4_HUMAN
33	212	29.8	136	1	RET3_HUMAN

34	210.5	29.6	137	1	RET3_XENLA	P50568 xenopus lae
35	210	29.5	136	1	RET3_MOUSE	P22695 mus musculus
36	204.5	28.8	137	1	RET4_MOUSE	P22935 mus musculus
37	204	28.7	136	1	RET3_FUGRU	O42386 fugu rubrip
38	196	27.6	130	1	FABP_BLOTA	O17284 blomia trop
39	193	27.1	138	1	RET4_RAT	P51673 rattus norv
40	190.5	26.8	133	1	FABP_SCHMA	P29498 schistosoma
41	184	25.9	131	1	FABP_LEPDS	Q9u5P1 lepidoglyph
42	182	25.6	120	1	RET3_CHICK	P40230 gallus gall
43	178	25.0	134	1	RET1_RAT	P02696 rattus norv
44	174	24.5	134	1	RET1_HUMAN	P09455 homo sapien
45	172	24.2	134	1	RET1_MOUSE	Q00915 mus musculus

ALIGNMENTS

RESULT 1
FABE_HUMAN STANDARD; PRT; 135 AA.
AC Q01469;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP).
GN FABP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Keratinocytes;
RX MEDLINE=92381332; PubMed=1512466;
RA Madsen P.S., Rasmussen H.H., Leffers H., Honore B., Celis J.E.;
RT "Molecular cloning and expression of a novel keratinocyte protein
RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
RT highly up-regulated in psoriatic skin and that shares similarity to
RT fatty acid-binding proteins.";
RL J. Invest. Dermatol. 99:299-305(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
RC TISSUE=Keratinocytes;
RX MEDLINE=94379963; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [4]
RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
RX MEDLINE=94379963; PubMed=8092987;
RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
RA Hellman U., Saurat J.-H.;
RT "Purification and characterization of the human epidermal fatty acid-
RT binding protein: localization during epidermal cell differentiation
RT in vivo and in vitro.";
RL Biochem. J. 302:363-371(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=99425110; PubMed=10493790;
RA Hohoff C., Borchers T., Rustow B., Spener F., van Tilbeurgh H.;
RT "Expression, purification and crystal structure determination of
RT recombinant human epidermal-type fatty acid-binding protein.";
RL Biochemistry 38:12229-12239(1999).
CC -1- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING


```

CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
CC EMBL; U13253; AAB86680.1; -.
CC EMBL; S69874; AAB30574.1; -.
CC EMBL; S83247; AAB46848.1; -.
CC HSSP; Q01469; 1B56.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding.
CC CONFLICT 49 49 G -> N (IN REF. 1).
CC CONFLICT 112 112 K -> N (IN REF. 3).
CC FT CONFLICT 112 112 K -> N (IN REF. 3).
CC SQ SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;

Query Match 85.9%; Score 611; DB 1; Length 135;
Best Local Similarity 81.1%; Pred. No. 8.3e-55;
Matches 110; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 MATVQQLGRLVDSKGFDEYMKELGVGLALRKMGMAMKPCDIITCDGKNLTIKTESTL 60
Db 1 MASLKDLGKRLVSHESPFEDYMKELGVGLALRKMGMAMKPCDIITLDGNNLVKTESTV 60
QY 61 KTTQFSCTLGEKEETADGRKGTQVCNFTDGLVQHQEWGDKESTITRKLKDGKLVVVC 120
Db 61 KTTVFSCTLGEKEETADGRKGTQVCNFTDGLVQHQEWGDKESTITRKLKDGKLVVVC 120
QY 121 VMNNVTCTRIYKVE 135
Db 121 VMNNAICTRIYKVVQ 135

RESULT 5
MYP2_RABIT
ID MYP2_RABIT STANDARD; PRT; 131 AA.
AC P02691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228063; PubMed=2453513;
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT "Characterization of a cloned cDNA encoding rabbit myelin P2
RT protein.";
RL J. Biol. Chem. 263:8332-8337(1988).
RN [2]
RP SEQUENCE OF 1-55.
RX MEDLINE=80094496; PubMed=7356651;
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin.";
RL J. Biol. Chem. 255:1058-1063(1980).
RN [3]
RP SEQUENCE OF 55-131.

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RX MEDLINE=82098098; PubMed=6172423;
RA Ishaque A., Hofmann T., Eylar E.H.;
RT "The complete amino acid sequence of the rabbit P2 protein.";
RL J. Biol. Chem. 257:592-595(1982).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
CC EMBL; J03744; AAA31451.1; -.
CC PIR; A03145; MPRB2.
CC PIR; A28081; A28081.
CC HSSP; P02690; 1PMP.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation.
CC INIT_MET 0 0 ACETYLTATION.
CC MOD_RES 1 1 E -> Q (IN REF. 3).
CC CONFLICT 72 72 E -> Q (IN REF. 3).
CC CONFLICT 83 83 I -> T (IN REF. 3).
CC CONFLICT 98 98 D -> N (IN REF. 3).
CC SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;

Query Match 56.5%; Score 402; DB 1; Length 131;
Best Local Similarity 61.1%; Pred. No. 9.6e-34;
Matches 77; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGLALRKMGMAMKPCDIITCDGKNLTIKTESTLKTQFSCT 68
Db 6 GTWKLVSSENFDDYMKALGVGLATRLKGLAKPNVVISKKGDIITIRTESTFKNTEISFK 65
QY 69 LGEKFEETADGRKGTQVCNFTDGLVQHQEWGDKESTITRKLKDGKLVVVCVNNVTCT 128
Db 66 LGOEFETADNRKTKSIITLGERGALNQVQKWDGKETTIRKLKLVGKVMVVECKMGVVC 125
QY 129 RYIEKV 134
Db 126 RYIEKV 131

RESULT 6
MYP2_HUMAN
ID MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;
RT "Isolation and sequence determination of cDNA encoding P2 protein of

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RT human peripheral myelin.";
RL Biochem. Biophys. Res. Commun. 181:204-207(1991).
RN [2]
RP SEQUENCE.
RX MEDLINE=83058785; PubMed=6183401;
RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
RL "The complete amino acid sequence of human P2 protein.";
RT J. Neurochem. 59:1759-1762(1982).
RN [3]
RP SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=95054012; PubMed=7525873;
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
RL Tennekoon G.;
RT "Partial structure and mapping of the human myelin P2 protein gene.";
RL J. Neurochem. 63:2010-2013(1994).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
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CC -----
DR EMBL; D16181; BAA03726.1; .
DR EMBL; D16179; BAA03726.1; JOINED.
DR EMBL; D16180; BAA03726.1; JOINED.
DR EMBL; X62167; CAA44096.1; .
DR EMBL; S73470; AAB32592.2; .
DR EMBL; S73468; AAB32592.2; JOINED.
DR EMBL; S73469; AAB32592.2; JOINED.
DR PIR; A03143; MP02.
DR PIR; J00977; J00977.
DR HSSP; P02690; 1PMP.
DR Genew; HGNC:9117; PMP2.
DR MIM; 170715; .
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0
FT MOD_RES 0 1 ACETYLTATION.
FT DISULFID 117 124
FT CONFLICT 24 24 G -> GG (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 2).
FT CONFLICT 110 110 N -> D (IN REF. 2).
SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Query Match 54.4%; Score 387; DB 1; Length 131;
Best Local Similarity 58.7%; Pred. No. 3;le-32;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTSTLTQFSCT 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKALCVGLATRLKGLNLAFTVIISKGDITIRTESTFKNTEISFK 65

QY 69 LGKEFEETADGRKTQTCVNFDTGALVQHQEWGDKRESTITRKLDGKLVVECVMNVTCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGQEFETADNRKTSIVTLQGRSLNQVQRWDGKETTITKRLVGMVAECKMKGVVCT 125

QY 129 RYIEKV 134
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 126 RYIEKV 131
```

```
RESULT 7
FABA_BOVIN STANDARD; PRT; 131 AA.
ID FABA_BOVIN STANDARD; PRT; 131 AA.
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
DE FABP4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartezko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers T., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89244; CAA61532.1; .
DR HSSP; P04117; 1LID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 19 19 BY SIMILARITY.
FT PHOSPHORYLTATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;

Query Match 53.7%; Score 382; DB 1; Length 131;
Best Local Similarity 56.8%; Pred. No. 1e-31;
Matches 71; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTSTLTQFSCT 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTSTLTQFSCT 65

QY 69 LGKEFEETADGRKTQTCVNFDTGALVQHQEWGDKRESTITRKLDGKLVVECVMNVTCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGQEFETADNRKTSIVTLQGRSLNQVQRWDGKETTITKRLKMDKMYLECMNGVTAT 125

QY 129 RYIEKV 133
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 126 RYIEKV 130

RESULT 8
MYP2_BOVIN STANDARD; PRT; 131 AA.
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80252120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine
RL peripheral nerve myelin.";
RT FEBS Lett. 115:27-30(1980).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RP MEDLINE=R9005045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBO J. 7:1597-1604(1988).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RP MEDLINE=G3253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic
RT transport proteins. Refinement of P2 myelin protein and the structure
RT determination and refinement of P2 myelin retinol-binding protein in
RL complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -I- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -I- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE FABP/P2/CRRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR PIR; A03144; MPB02.
DR PDB; 1PW6; 26-JAN-95.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATPYACIDBP.
DR PROSITE; PS00214; FATTY_1.
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
FT MOD_RES 1 1 ACETYLATION.
FT DSULFID 117 124
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 53.7%; Score 382; DB 1; Length 131;
Best Local Similarity 58.7%; Pred. No. le-31;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps

QY 9 GRWRVLDSKGFEDYMKELVGIALRMKGAMAKPCDIITCDCKNLTKTESTLKTTFQSCT 68
| : | | | : | | | | | | | | | : | | | : | : | | | | | : | |
Db 6 GTWKLVSSSENFDEYMKALGVGLATRKLNLAAPRVISKSGKDIIITIESPFKNTELSPK 65
| : | | | | | | | | | : | : | | | | | | | | | | | | | | | : | |
QY 69 LGKFEBETTADGRKQTVCNFTFDGALVQHOMDGKESITTRKLXDKGLVECYVMNNVTCT 128
| : | | | | | | | | | : | : | | | | | | | | | | | | | | | : | |
Db 66 LGQFEFTTADRNRKTSVTTLARGSLNQVKWNGNETTIKRKLVDGMKVYECKMDVVCT 125
| : | | | | | | | | | : | : | | | | | | | | | | | | | | | : | |

QY 129 RIYEKV 134
| | | | |
Db 126 RIYEKV 131
| | | | |

RESULT 9
FABA_PIG
ID_FABA_PIG STANDARD; PRT; 131 AA.
AC Q97788;
DT 16-OCT-2001 (Rel. 40, Created)


```
RESULT 10
MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
TRANSPORTERS.
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CC -----
CC EMBL; S39508; AAB19249.2; -.
DR PIR; JH0407; JH0407.
DR HSP; P02690; IPMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; LipocIn_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;
Query Match 52.5%; Score 373; DB 1; Length 131;
Best Local Similarity 55.6%; Pred. No. 8 1e-31;
Matches 70; Conservative 22; Mismatches 34; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVIALRMGAMAKPDCIITCDGKNLTKITESTLKTQFSCT 68
Db 6 GTWKLVSSSEHFDYMKALGVLANRKLGNLAKPTVIISKKGDYITRTESAPKNTSEIFK 65
QY 69 LGKKEFTETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDLGVVCEYVNNVTCT 128
Db 66 LGQEFDETTADNRKAKSVITVLGRGSLQVQKWDGKETARRLLDGRMVVECMKGVCVT 125
QY 129 RYIEKV 134
Db 126 RYIEKV 131
RESULT 11
FABA_SPETR
ID FABA_SPETR STANDARD; PRT; 131 AA.
AC Q99P60;
DT 15-JUN-2002 (Rel. 41, Created)
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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
protein) (ALBP) (A-FABP).
GN FABP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittell D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding
proteins in hibernating ground squirrels.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CHAIN FATTY ACID AND RETINOIC ACID (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
TRANSPORTERS.
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CC -----
CC EMBL; AF327855; AAK08084.1; -.
DR HSP; P04117; ILID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; LipocIn_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
(BY SIMILARITY).
SQ SEQUENCE 131 AA; 14634 MW; FCEE7B092A2AF708 CRC64;
Query Match 52.2%; Score 371; DB 1; Length 131;
Best Local Similarity 55.2%; Pred. No. 1.3e-30;
Matches 69; Conservative 23; Mismatches 33; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVIALRMGAMAKPDCIITCDGKNLTKITESTLKTQFSCT 68
Db 6 GTWKLVSSSEHFDYMKELGVIALRMGAMAKPDCIITCDGKNLTKITESTLKTQFSCT 65
QY 69 LGKKEFTETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDLGVVCEYVNNVTCT 128
Db 66 LGQEFDETTADNRKAKSVITVLGRGSLQVQKWDGKETARRLLDGRMVVECMKGVCVT 125
QY 129 RYIEK 133
Db 126 RYIEK 130
RESULT 12
FABA_HUMAN
ID FABA_HUMAN STANDARD; PRT; 131 AA.
AC P15090;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
protein) (ALBP) (A-FABP).
GN FABP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105397; PubMed=2481498;
RA Baxa C.A., Sha R.S., Buel M.K., Smith A.J., Matarese V.,
RA Chinander L.L., Boundy K.L., Bernlohr D.A.;
RT "human adipocyte lipid-binding protein: purification of the protein
RL and cloning of its complementary DNA.";
RL Biochemistry 28:8683-8690(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=urinary bladder;
RA Scrausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02874; AAA51689.1; -
DR EMBL: BC003672; AAH03672.1; -
DR PIR: A33363; A33363.
DR HSP: P04117; LLID.
DR Genew: HGNC:3559; FABP4.
DR MIM: 600434; -
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocin_cyFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;
Query Match 51.5%; Score 366; DB 1; Length 131;
Best Local Similarity 55.2%; Pred. No. 4.1e-30;
Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKGAMAKPDGCIITCDGKNLTIKTESTLTKTTFQSCF 68
DB 6 GTWKLVSSSEFDDYMKVEGVGATRKVACMAKPNMIISVNGVDVITKSESTKNTFISFI 65
QY 69 LGEKPEETADRGKTQTVCNFTDGLVQHOEWGDKRESTTRKLDGKLVVECMNVNVTCT 128
DB 66 LGQEFDEVTDARKVKSTITLDGGVLVHVQKWDGKSTTIKRRKREDKLVVECMKGVST 125
QY 129 RIVEK 133
DB 126 RYER 130
RESULT 13
FABA_MOUSE
ID FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DE 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (FABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (P2 adipocyte protein) (Myelin P2 protein
DE homolog) (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RL identification of an mRNA encoding a homologue of myelin P2
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233319; PubMed=3520554;
RA Hunt C.R., Ro J.H.-S., Dobson D.E., Min H.Y., Spiegelman B.M.;
RT "Adipocyte P2 gene: developmental expression and homology of
RL 5'-flanking sequences among fat cell-specific genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278164; PubMed=3015943;
RA Phillips M., Djan P., Green H.;
RT "The nucleotide sequence of three genes participating in the adipose
RL differentiation of 3T3 cells.";
RL J. Biol. Chem. 261:10821-10827(1986).
RN [4]
RP SEQUENCE
RX MEDLINE=89008309; PubMed=2844775;
RA Matarese V., Bernlohr D.A.;
RT "Purification of murine adipocyte lipid-binding protein.
RL Characterization as a fatty acid- and retinoic acid-binding
RL protein.";
RL J. Biol. Chem. 263:14544-14551(1988).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momaberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=88203618; PubMed=2452440;
RA Cook J.S., Lucas J.J., Sibley E., Bolanowski M.A., Christy R.J.,
RA Kelly T.J. Jr., Lane M.D.;
RT "Expression of the differentiation-induced gene for fatty acid-binding
RL protein is activated by glucocorticoid and cAMP.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).
RN [7]
RP SEQUENCE OF 10-131 FROM N.A.
RX MEDLINE=85105214; PubMed=3968175;
RA Cook K.S., Hunt C.R., Spiegelman B.M.;
RT "Developmentally regulated mRNAs in 3T3-adipocytes: analysis of
RL transcriptional control.";
RL J. Cell Biol. 100:514-520(1985).

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RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=92207973; PubMed=1554730;
 RA Xu Z., Bernlohr D.A., Banaszak L.J.;
 RT "Crystal structure of recombinant murine adipocyte lipid-binding
 protein.";
 RL Biochemistry 31:3484-3492(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=93216758; PubMed=8463311;
 RA Xu Z., Bernlohr D.A., Banaszak L.J.;
 RT "The adipocyte lipid-binding protein at 1.6-A resolution. Crystal
 structures of the apoprotein and with bound saturated and unsaturated
 fatty acids.";
 RL J. Biol. Chem. 268:7874-7884(1993).
 CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
 CC CHAIN FATTY ACID AND RETINOIC ACID.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CBPP/CBAP FAMILY OF
 CC TRANSPORTERS.
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 CC -----
 DR EMBL: K02109; AAA39416.1; -;
 DR EMBL: M13264; AAA39870.1; -;
 DR EMBL: M13261; AAA39870.1; JOINED.
 DR EMBL: M13262; AAA39870.1; JOINED.
 DR EMBL: M13263; AAA39870.1; JOINED.
 DR EMBL: M13385; AAA39417.1; -;
 DR EMBL: AK003143; BAB22601.1; -;
 DR EMBL: M20497; AAA37188.1; -;
 DR EMBL: M28726; AAA37112.1; -;
 DR PIR: A05089; A05089.
 DR PIR: A24884; A24884.
 DR PIR: A30810; A30810.
 DR PIR: B25952; B25952.
 DR PDB: 1ALB; 31-OCT-93.
 DR PDB: 1LIB; 30-APR-94.
 DR PDB: 1LIC; 30-APR-94.
 DR PDB: 1LID; 30-APR-94.
 DR PDB: 1LIE; 30-APR-94.
 DR PDB: 1LIF; 30-APR-94.
 DR PDB: 1ADL; 20-DEC-94.
 DR PDB: 1AB0; 16-JUN-97.
 DR PDB: 1ACD; 16-JUN-97.
 DR PDB: 1A18; 01-JUL-98.
 DR PDB: 1A2D; 01-JUL-98.
 DR SWISS-2DPAGE: P04117; MOUSE.
 DR MGD: MGI:88038; Fabp4.
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PS00178; FATTYACIDBP.
 DR PROSITE: PS00214; FABP; 1.
 KW Transport; Lipid-binding; Phosphorylation; 3D-structure.
 FT INIT_MET 0
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
 FT FT
 FT CONFLICT 39 39 (BY SIMILARITY).
 FT CONFLICT 110 110 N -> T (IN REF. 2; AAA39870).
 FT HELIX 2 4 G -> V (IN REF. 3; AAA39417).
 FT STRAND 6 14
 FT HELIX 16 23
 FT TURN 24 24
 FT TURN 27 35
 FT STRAND 39 45
 FT TURN 46 47

FT STRAND 48 54
 FT TURN 59 64
 FT TURN 66 67
 FT STRAND 70 73
 FT TURN 75 76
 FT STRAND 79 87
 FT TURN 88 89
 FT STRAND 90 97
 FT TURN 98 99
 FT STRAND 100 109
 FT TURN 110 111
 FT STRAND 112 119
 FT TURN 120 121
 FT STRAND 122 130
 SQ SEQUENCE 131 AA; 14519 MW; ED57D4E2774B8E32 CRC64;
 Query Match 50.6%; Score 360; DB 1; Length 131;
 Best Local Similarity 55.2%; Pred. No. 1.7e-29;
 Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAAPKDCIITCDGKNLTIKTTESTLKTTFQSCT 68
 Db 6 GTWKLVSSSENFDDYMKVEGVGFATRKVAGMAKPNMIIISVNGDLVTIRSESTFKNTEISFK 65
 QY 69 LGEKPEETADGRKTQTVCNFTDGCALVQHQEWGDKESTITRKLDKGLVVECVNNTCT 128
 Db 66 LGVEFDEITADGRKVKSIITLDGGLVQVQKWDGKSTTKRKRDGDKLVVECVNMTST 125
 QY 129 RIVEK 133
 Db 126 RVIER 130
 RESULT 14
 FABH_RAT STANDARD; PRT; 132 AA.
 AC P07483; Q9QY04;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fatty acid-binding protein, heart (H-FABP).
 GN FABP3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250640; PubMed=3036869;
 RA Heuckeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
 RT "Analysis of the tissue-specific expression, developmental
 RT regulation, and linkage relationships of a rodent gene encoding heart
 RT fatty acid binding protein.";
 RL J. Biol. Chem. 262:9709-9717(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88107756; PubMed=3427112;
 RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
 RT "Cloning and tissue distribution of rat heart fatty acid binding
 RT protein mRNA: identical forms in heart and skeletal muscle.";
 RL Biochemistry 26:7900-7904(1987).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=88153733; PubMed=3162235;
 RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
 RT "Revision of the blocked N terminus of rat heart fatty acid-binding
 RT protein by liquid secondary ion mass spectrometry.";
 RL J. Biol. Chem. 263:4182-4185(1988).
 RN [4]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE=86250713; PubMed=2424895;
 RA Sacchettini J.C., Said B., Schulz H., Gordon J.I.;
 RT "Rat heart fatty acid-binding protein is highly homologous to the


```

FT  MOD_RES      1      1      ACETYLLATION.
FT  MOD_RES     19     19      PHOSPHORYLATION (BY TYR-KINASES)
FT                                     (POTENTIAL).
SQ  SEQUENCE    132 AA; 15079 MW; 2AFDEA2C0BE2095F CRC64;

Query Match      48.4%; Score 344; DB 1; Length 132;
Best Local Similarity 51.6%; Pred. No. 6.9e-28;
Matches 66; Conservative 18; Mismatches 44; Indels 0; Gaps 0;

QY  4  VQOLEGRWRLVDSKGFDEYMKELGVGIALRKMAMAKPCDIITCDGKNLTIKTESTLKT 63
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  1  VEAFLGSKWLQKSHNFDEYMKNLDSLAQRKVATTVKPKTIISLDGDVITIKTESTFKST 60

QY  64  QFSCTLGEKFEETTADGRKTQVCNFTDGA LVQHOEWDGKESTITRKLKDGKLVVECVMN 123
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  61  NIQFKLAEEFDETTADNRRTTKTVKLENGKLVQTORWDGKETT LVRELQDGKLIILTCTMG 120

QY  124  NVTCTRIY 131
    | : | | | | |
Db  121  DVVCTREY 128
    | : | | | | |

```

Search completed: November 25, 2002, 10:35:30
Job time : 13 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:33:23 : Search time 17 Seconds
(without alignments)
763.420 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVQLEGRLVDSKGF.....LVVECMNVCTRIYEKVE 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	2 I56326	fatty acid binding
2	612	86.1	135	2 A47497	lipid-binding prot
3	611	85.9	135	2 JC2201	fatty acid-binding
4	402	56.5	132	1 MPRB2	myelin P2 protein
5	387	54.4	132	1 MPHU2	myelin P2 protein
6	382	53.7	131	1 MPB02	myelin P2 protein
7	382	53.7	132	2 S57744	adipocyte-type fat
8	373	52.5	132	2 JH0407	myelin P2 protein
9	366	51.5	132	1 FZHU6	fatty acid-binding
10	358	50.4	132	2 B25952	myelin P2 protein
11	344	48.4	132	2 S20297	fatty acid-binding
12	344	48.4	133	2 A27452	fatty acid-binding
13	337	47.4	133	1 FZHU6	fatty acid-binding
14	331	46.6	133	2 A34676	fatty acid-binding
15	326	45.9	133	2 PC4011	fatty acid-binding
16	319	44.9	132	2 I52524	testis lipid bindi
17	308	43.3	131	2 S08479	fatty acid-binding
18	307	43.2	132	2 A49184	fatty acid-binding
19	304	42.8	132	2 I58161	lipid-binding prot
20	304	42.8	132	2 I48923	fatty acid-binding
21	303	42.6	132	2 I56510	fatty acid binding
22	234.5	33.0	135	2 T15205	hypothetical prote
23	231.5	32.6	137	2 T21203	hypothetical prote
24	224.5	31.6	136	2 T15207	hypothetical prote
25	214.5	30.2	138	1 RJHU1	retinoic acid-bind
26	212	29.8	137	1 RJHU2	retinoic acid-bind
27	210.5	29.6	138	2 A2495	retinoic acid-bind
28	210.5	29.6	138	2 I51265	xCRABP - African c
29	210	29.5	137	1 RJBOA	retinoic acid-bind

30	210	29.5	137	2 A35825	retinoic acid-bind
31	201.5	28.3	133	2 A48578	fatty acid-binding
32	193	27.1	139	2 I53298	cellular retinoic
33	190.5	26.8	133	2 A39818	14K fatty acid-bin
34	187.5	26.4	134	2 S29600	fatty acid-binding
35	178	25.0	135	1 RJRTO	retinol-binding pr
36	174	24.5	135	1 RJHU0	retinol-binding pr
37	172	24.2	135	2 S16355	retinol-binding pr
38	171	24.1	95	2 A61629	retinoic acid-bind
39	171	24.1	134	2 S43470	fatty acid-binding
40	168	23.6	133	2 A44870	fatty acid-binding
41	162	22.8	134	2 S69360	retinol-binding pr
42	159	22.4	134	2 S34717	retinol-binding pr
43	155	21.8	134	2 A29065	retinol-binding pr
44	154	21.7	100	2 S13796	retinoic acid-bind
45	153	21.5	132	2 I51450	fatty acid binding

ALIGNMENTS

RESULT 1

I56326
fatty acid binding protein homolog - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I56326
R.Madsen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Cellis, J.E.
J. Invest. Dermatol. 99, 299-305, 1992
A>Title: Molecular cloning and expression of a novel keratinocyte protein (psoriasis-
ilality to fatty acid-binding proteins.
A:Reference number: I56326; MUID:92381332; PMID:1512466
A:Accession: I56326
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-135 <RES>
A:Cross-references: GB:M94856; NID:gl82353; PIDN:AAA58467.1; PID:gl82354
C:Genetics:
A:Gene: PA-FABP
C:Superfamily: myelin P2 protein

Query Match 100.0%; Score 711; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 4.4e-61; Indels 0; Gaps 0;
Matches 135; Conservative 0; Mismatches 0;

QY 1 MATVQLEGRLVDSKGFDEYMKELGVIALRKMGMARPDCCIITCDGKNLIKTESTL 60
|||||

Db 1 MATVQLEGRLVDSKGFDEYMKELGVIALRKMGMARPDCCIITCDGKNLIKTESTL 60
|||||

QY 61 KTFQFSCITLGEKEFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVEEC 120
|||||

Db 61 KTFQFSCITLGEKEFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVEEC 120
|||||

QY 121 VMNNVTCTRIYEKVE 135
|||||

Db 121 VMNNVTCTRIYEKVE 135
|||||

RESULT 2

A47497
lipid-binding protein, keratinocyte - mouse
N:Alternate names: lipid-binding protein mall
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999
C:Accession: A47497; S36635
R.Krieg, P.; Fell, S.; Fuerstenberger, G.; Bowden, G.T.
J. Biol. Chem. 268, 17362-17369, 1993
A>Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.
A:Reference number: A47497; MUID:93352523; PMID:8349619
A:Accession: A47497
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-135 <KRI>
A:Cross-references: EMBL:X70100; NID:g287985; PIDN:CAA49703.1; PID:g287986
C:Superfamily: myelin P2 protein

Query Match 86.1%; Score 612; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 1.4e-51;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESL 60

Db 1 MASLKDEGKRWLVESHGFEYMKELGVGLALRKMAAMKPCDIITCDGNITIVKTESTV 60

QY 61 KTTQFSCITLGEKFEETADGRKTQTCVNETDQALVQHQEWGDKESIITRKLKDGKLVVVC 120

Db 61 KTTVFSCNLGKPFDETTADGRKTETVCTFDQDALVQHQWQDKESIITRKLKDGKLVVVC 120

QY 121 VMNNVTCTRIYEKVE 135

Db 121 VMNNATCTRYEKVQ 135

RESULT 3

JC2201

fatty acid-binding protein, cutaneous - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-2000

C:Accession: JC2201; JC7377

R:Watanabe, R.; Fujii, H.; Odani, S.; Sakakibara, J.; Yamamoto, A.; Ito, M.; Ono, T.

Biochem. Biophys. Res. Commun. 200, 253-259, 1994

A:Title: Molecular cloning of a cDNA encoding a novel fatty acid-binding protein from rat

A:Reference number: JC2201; MUID:94220094; PMID:8166694

A:Accession: JC2201

A:Molecule type: mRNA

A:Residues: 1-135 <KAT>

A:Cross-references: GB:S69874; NID:g546419; PIDN:AAB30574.1; PID:g546420

R:Odani, S.; Namba, Y.; Ishii, A.; Ono, T.; Fujii, H.

J. Biochem. 128, 355-361, 2000

A:Title: Disulfide bonds in rat cutaneous fatty acid-binding protein.

A:Reference number: JC7377

A:Contents: Skin

A:Accession: JC7377

A:Molecule type: mRNA

A:Residues: 1-135 <ODA>

C:Comment: This protein is involved in intracellular transport and metabolism of fatty a

F:22/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predi

C:Genetics:

A:Gene: c-fabp

C:Superfamily: myelin P2 protein

C:Keywords: cutaneous gland; disulfide bond; phosphoprotein; skin

F:109/Binding site: fatty acid (Arg) #status predicted

Query Match 85.9%; Score 611; DB 2; Length 135;

Best Local Similarity 81.5%; Pred. No. 1.7e-51;

Matches 110; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESL 60

Db 1 MASLKDEGKRWLVESHGFEYMKELGVGLALRKMGAMAKPDCIITCDGNITIVKTESTV 60

QY 61 KTTQFSCITLGEKFEETADGRKTQTCVNETDQALVQHQEWGDKESIITRKLKDGKLVVVC 120

Db 61 KTTVFSCNLGKPFDETTADGRKTETVCTFDQDALVQHQWQDKESIITRKLKDGKLVVVC 120

QY 121 VMNNVTCTRIYEKVE 135

Db 121 VMNNATCTRYEKVQ 135

RESULT 4

MFRB2

myelin P2 protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
A:Accession: A28081; A92266; A92372; A03145
R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.

J. Biol. Chem. 263, 8332-8337, 1988

A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.

A:Reference number: A28081; MUID:88228063; PMID:2453513

A:Accession: A28081

A:Molecule type: mRNA

A:Residues: 1-132 <NAR>

A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658

A:Note: translation of initiator Met is not shown

R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.

J. Biol. Chem. 255, 1058-1063, 1980

A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.

A:Reference number: A92266; MUID:80094496; PMID:7356651

A:Accession: A92266

A:Molecule type: protein

A:Residues: 2-56 <ISL>

R:Ishaque, A.; Hofmann, T.; Eylar, E.H.

J. Biol. Chem. 257, 592-595, 1982

A:Title: The complete amino acid sequence of thr rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423

A:Accession: A92372

A:Molecule type: protein

A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction o

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status predicted

Query Match 56.5%; Score 402; DB 1; Length 132;

Best Local Similarity 61.1%; Pred. No. 1.9e-31;

Matches 77; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTOFSC 68

Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLPVLSKKGDIITRTSTFKNTSISK 66

QY 69 LGKEPSETTADGRKTQTCVNETDQALVQHQEWGDKESIITRKLKDGKLVVVCVMNNVTCT 128

Db 67 LGQEFETTADNRKTSIITLBERGALNQVQKWDGKETTKRKLVDGKMVVECKMKGVCT 126

QY 129 RIYEKV 134

Db 127 RIYEKV 132

RESULT 5

MPHU2

myelin P2 protein [validated] - human

N:Alternate names: peripheral myelin protein 2

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000

C:Accession: J70977; A03143; S24224

R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human pe

A:Reference number: J70977; MUID:92068191; PMID:1720307

A:Accession: J70977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A:Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98,'N',100-110,'D',112-132 <SUZ>

A;Reference number: S57744
A;Accession: S57744
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-132 <SPE>
A;Cross-references: EMBL:X89244; NID:g895753; PIDN:CRA61532.1; PID:g895754
C;Superfamily: myelin P2 protein

Query Match 53.7%; Score 382; DB 2; Length 132;
Best Local Similarity 56.8%; Pred. No. 1.5e-29;
Matches 71; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGAMAKPCIITCDGKNLTIKTESTLKTPQSCT 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 GTWKLVSSEHFDYMKEGVGFGATRKVAGMAKPTLIISLNGVVVTIKSESTFKNTEISFK 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 69 LGKEFEETTAGRKTQVCNFDTGALVQHGEWDGKESTITRKLKDGLVVECVNNVTCT 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 67 LGOEFDEITPDRKVKSIVNLDEGALVQVONWDGKSTTKRKLMDDKRVLECVNWGYTAT 126
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 129 RIVEK 133
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 127 RVYEK 131
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
JH0407
myelin p2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change_13-Aug-1999
C;Accession: JH0407
R;Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 75-80, 1991
A;Title: Structure of the mouse myelin P2 protein gene.
A;Reference number: JH0407; MUID:91268811; PMID:1711100
A;Accession: JH0407
A:Molecule type: DNA
A;Residues: 1-132 <NAR>
A;Cross-references: GB:S39508; NID:g232319; PIDN:AAB19249.1; PID:g232320
C;Comment: This basic protein is found in peripheral and central nervous system myelin.
C;Genetics:
A;Introns: 25/1; 82/3; 116/3
C;Superfamily: myelin P2 protein

Query Match 52.5%; Score 373; DB 2; Length 132;
Best Local Similarity 55.6%; Pred. No. 1.1e-28;
Matches 70; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGAMAKPCIITCDGKNLTIKTESTLKTPQSCT 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 GTWKLVSSEHFDYMKALGVLANRLGNLAKPTVIISKGGDYITIRTSFAFNTEISFK 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 69 LGKEFEETTAGRKTQVCNFDTGALVQHGEWDGKESTITRKLKDGLVVECVNNVTCT 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 67 LGOEFDEITADNRKAISVTLERGSVKQVQWDGKETAIRRTLLDGRMVVECMKGVVCT 126
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 129 RIVEK 134
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 127 RIVEK 132
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
FZHUFL
fatty acid-binding protein, adipocyte - human
N;Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein
C;Species: Homo sapiens (man)
C;Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C;Accession: A33363
R;Baxa, C.A.; Sha, R.S.; Buelt, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Bou
Biochemistry 28, 8693-8690, 1989
A;Title: Human adipocyte lipid-binding protein: purification of the protein and cloni
A;Reference number: A33363; MUID:90105397; PMID:2481498
A;Accession: A33363

C: Superfamily: myelin p2 protein
C: Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
F: 1-133/Product: fatty acid-binding protein #status experimental <NAT>
F: 1/Modified site: acetylated amino end (Met) #status predictedF: ..

Query Match 48.4%; Score 344; DB 2: Length 133;
Best Local Similarity 52.8%; Pred. No. 6.9e-26;
Matches 66; Conservative 19; Mismatches 40; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKGMAMAKPDCIITCDGKNLTITKSTLKTQFSCT 68
| : | | | | | : | | | | | : | : | | | | | : | : | | | | | : |
Db 7 GTWKLVDSKFNDDYMKSLGSGVGFATQVASMTPKPTTIIKNGDPTTIKTHSTFKNTEISFQ 66
| : | | | | | : | | | | | : | : | | | | | : | : | | | | | : |

QY 69 LGSKFEBTTADGRKQTQVCFNTGALVHOHEWGDKESTITRKLDKGLVCECVNNVTCT 128
| : | : | | | | | : | | | | | : | : | | | | | : | : | | | | | : |
Db 67 LGVEFDEVTAADRRKRVSVVTLDGGLKLVHQWGDQETTLRELSDGKLILTLTHGNVYST 126
| : | | | | | : | | | | | : | : | | | | | : | : | | | | | : |

QY 129 RYEK 133
| | | | |
Db 127 RYEK 131
| | | | |

RESULT 13
F2HUUC
fatty acid-binding protein, cardiac and skeletal muscle - human
N: Alternate names: fatty acid-binding protein 3 (FABP3)
C: Species: Homo sapiens (man)
C: Date: 30-Jun-1991 #sequence_revision 03-May-1996 #text_change 16-Jul-1999
C: Accession: S15432; JH0199; S00603; I54275; A27248
R: Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
Biochem. J. 276, 203-207, 1991
A: Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protein
A: Reference number: S15432; MUID: 91248148; PMID: 1710107
A: Accession: S15432
A: Molecule type: mRNA; protein
A: Residues: 1-133 <PEE>
A: Cross-references: EMBL: X56549; NID: g31292; PIDN: CAA39889.1; PID: g31293
R: Boerchers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
Mol. Cell. Biochem. 98, 127-133, 1990
A: Title: Revision of the amino acid sequence of human heart fatty acid-binding protein
A: Reference number: JH0199; MUID: 91094793; PMID: 2266954
A: Accession: JH0199
A: Molecule type: protein
A: Residues: 2-129, 'Q', 131-133 <BOE>
R: Offner, G.D.; Brecher, P.; Sawilivich, W.B.; Costello, C.E.; Troxler, R.F.
Biochem. J. 252, 191-198, 1988
A: Title: Characterization and amino acid sequence of a fatty acid-binding protein from
A: Reference number: S00603; MUID: 88339792; PMID: 3421901
A: Accession: S00603
A: Molecule type: protein
A: Residues: 2-104, 'K', 106-124, 'S', 126-133 <OFF>
A: Note: submitted to the Protein Sequence Database, May 1988
R: Zanotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
J. Biol. Chem. 267, 18341-18550, 1992
A: Title: Three-dimensional structure of recombinant human muscle fatty acid-binding p
A: Reference number: A49251; MUID: 92406763; PMID: 1526991
A: Contents: annotation: X-ray crystallography, 2.1 angstroms
A: Note: recombinant protein expressed in Escherichia coli
R: Troxter, R.F.; Offner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Milunsky, A.; Wyan
Hum. Genet. 92, 563-566, 1993
A: Title: Localization of the gene for human heart fatty acid binding protein to chrom
A: Reference number: I54275; MUID: 94085953; PMID: 8262516
A: Accession: I54275
A: Status: translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 15-133 <RES>
A: Cross-references: GB: S67314; NID: g458861; PIDN: AAB29294.1; PID: g458862
C: Genetics:
A: Gene: GDB: FABP3
A: Cross-references: GDB: 128008; OMIM: 134651
A: Map position: lp33-lp32
C: Superfamily: myelin p2 protein

017 120 PIVEK 123

On 170 p. 123

Db 127 RTYK 131

Search completed: November 25, 2002, 10:35:54
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:35:18 ; Search time 10 Seconds
(without alignments)
211.430 Million cell updates/sec

Title: US-09-788-074-3

Perfect score: 711

Sequence: 1 MATVQLEGRLVDSKGFD.....LVCEVMNNVTCTRIYEKVE 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	711	100.0	135	10	US-09-788-074-3
2	612	86.1	135	10	US-09-788-074-1
3	387	54.4	132	10	US-09-901-436A-11
4	366	51.5	132	10	US-09-905-235-1
5	337	47.4	132	10	US-09-986-240-2
6	337	47.4	133	10	US-09-901-436A-10
7	337	47.4	133	12	US-10-153-740-13
8	331	46.6	133	12	US-10-153-740-12
9	326	45.9	133	10	US-09-901-436A-7
10	326	45.9	133	12	US-10-153-740-11
11	303	42.6	132	10	US-09-971-187-2
12	291.5	41.0	131	12	US-10-153-740-15
13	223.5	31.4	149	10	US-09-925-302-496
14	214.5	30.2	138	9	US-09-736-457-328
15	195	27.4	160	10	US-09-925-301-848
16	174	24.5	135	10	US-09-901-436A-8
17	168	23.6	135	10	US-09-737-149-48
18	168	23.6	135	10	US-09-737-149-49
19	168	23.6	135	12	US-10-153-740-2

20	167	23.5	135	10	US-09-737-149-16	Sequence 16, Appl
21	136	19.1	156	10	US-09-737-149-14	Sequence 14, Appl
22	132	18.6	134	10	US-09-901-436A-9	Sequence 9, Appl
23	118	16.6	107	10	US-09-901-436A-2	Sequence 2, Appl
24	112.5	15.8	106	12	US-10-153-740-14	Sequence 14, Appl
25	110	15.5	70	10	US-09-737-149-46	Sequence 46, Appl
26	110	15.5	70	10	US-09-737-149-47	Sequence 47, Appl
27	94.5	13.3	127	9	US-09-981-353-21	Sequence 21, Appl
28	83	11.7	26	10	US-09-347-064-14	Sequence 14, Appl
29	76.5	10.8	98	10	US-09-925-299-1198	Sequence 1198, Ap
30	75	10.5	997	10	US-09-747-371-3	Sequence 3, Appl
31	73	10.3	758	10	US-09-903-248-2	Sequence 2, Appl
32	73	10.3	758	10	US-09-859-604-2	Sequence 2, Appl
33	73	10.3	758	10	US-09-903-063-2	Sequence 2, Appl
34	73	10.3	758	10	US-09-903-216-2	Sequence 2, Appl
35	73	10.3	758	10	US-09-903-199-2	Sequence 2, Appl
36	73	10.3	758	10	US-09-903-023-2	Sequence 2, Appl
37	69	9.7	343	10	US-09-815-242-5512	Sequence 5512, Ap
38	69	9.7	343	10	US-09-815-242-12152	Sequence 12152, A
39	69	9.7	1477	9	US-10-092-880-4	Sequence 4, Appl
40	68	9.6	614	10	US-09-782-051-2	Sequence 2, Appl
41	65.5	9.2	1426	10	US-09-912-020-340	Sequence 340, App
42	65	9.1	180	9	US-09-818-648-1	Sequence 1, Appl
43	65	9.1	180	10	US-09-828-217-1	Sequence 1, Appl
44	65	9.1	180	10	US-09-760-723-5	Sequence 5, Appl
45	65	9.1	180	10	US-09-355-925-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-788-074-3
; Sequence 3, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Hotamisligil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MALL
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-074-3

Query Match	100.0%	Score 711;	DB 10;	Length 135;
Best Local Similarity	100.0%	Pred No. 1.3e-70;		
Matches 135;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MATVQLEGRLVDSKGFDYMKELGVGIALRKMGA	PKDCIITCDGKNLTKTESTL	60
Db	1	MATVQLEGRLVDSKGFDYMKELGVGIALRKMGA	PKDCIITCDGKNLTKTESTL	60
QY	61	KITQFSCITLGEKEFEETADGRKTQTCVNF	TGALVQHQEWGDKESTITRKLKDGKLWVEC	120
Db	61	KITQFSCITLGEKEFEETADGRKTQTCVNF	TGALVQHQEWGDKESTITRKLKDGKLWVEC	120
QY	121	VMNNVTCTRIYEKVE	135	
Db	121	VMNNVTCTRIYEKVE	135	
RESULT 2				
US-09-788-074-1				
; Sequence 1, Application US/09788074				
; Patent No. US20010044110A1				
; GENERAL INFORMATION:				

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; APPLICANT: Hotamisliligil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MAL1
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 135
; TYPE: prt
; ORGANISM: Mus musculus
US-09-788-074-1

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Query Match	86.1%	Score 612;	DB 10;	Length 135;
Best Local Similarity	80.0%;	Pred. No. 7.9e-60;		
Matches 108;	Conservative 18;	Mismatches 9;	Indels 0;	Gaps 0;
QY	1	MATVQQLGGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCITCDGKNLTIKTESTL	60	
Db	1	MAKLDLEGKRWLRMESHGFEEYMKELGVGLALRKMAAMAKPDCITCDGNNITVKTESTV	60	
QY	61	KTTQFSCTLGEKFEETTTADGRKKTQVCFNFTDQALVQHQEWQDGKESTITRKLKDGLVVEEC	120	
Db	61	KTIVFSNLGEKFEETTTADGRKTEVCTFDQALVQHQEWQDGKESTITRKLKDGMIVVEEC	120	
QY	121	VMNNVTCTRIYKEVE	135	
Db	121	VMNNATCTRIYKEVQ	135	

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RESULT 3
US-09-901-436A-11
; Sequence 11, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF175D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-11

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Query Match	54.4%	Score	387	DB	10	Length	132
Best Local Similarity	58.7%	Pred. No.	2.6e-35				
Matches	74	Conservative	19	Mismatches	33	Indels	0
Gaps	0						
QY	9	GRWLVDKSGFDEVMKELGVGIALRKKAMAKPCDIITCDCKNLTIKTESTLKTQPSCT	68				
DB	7	GTWKLVSSEFDDYMKALGVGLATRKLGNLAKPVIISKKGDIITITESTFKKNTETSK	66				
QY	69	LGKFEFTTADGRKTQVCFNTDGAALVQHEWDGKESTITRKLDDGKLIVCEVMNNVTCT	128				
DB	67	LGQFEFTTADNRKTSIVTLQRGSLNQVQRWDGKETITRKLVLNGKMAECKMKGVVCT	126				
QY	129	RIYEKV	134				
DB	127	RIYEKV	132				

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RESULT 4
US-09-905-235-1
: Sequence 1, Application US/09905235
: Patent No. US2002035064A1
: GENERAL INFORMATION:
: APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
: TITLE OF INVENTION: METHOD FOR TREATING D
: FILE REFERENCE: LA24a
: CURRENT APPLICATION NUMBER: US/09/905,235
: CURRENT FILING DATE: 2001-07-13
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 132
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-905-235-1

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Qy	9	GRRLVDSKGDEYNKELGVGIALRKKMGAMAKPDCIIITCDGKNLTIKTESTLTKTTQFSCT	68		
	1				
	7	GTWKLVSSEFDDYMKVEGVFATRKVAGMAKPNMIIISVNGDVITIKSESTFKNTEISFI	66		
Db					
Qy	69	LGEAFEEITADGRKTQTCVNTDTCALVQHQEWDGKSEITIRKLKGKLVWECVMNNVTCT	128		
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Db	67	LGQBFDEVTADRRVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVWECVMKGVST	126		
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RESULT 5
US-09-986-240-2
; Sequence 2, Application US/09986240
; Patent No. US2002011946A1
; GENERAL INFORMATION:
; APPLICANT: Weigelt, Johan
; APPLICANT: Wikström, Mats
; TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 13425-047001
; CURRENT APPLICATION NUMBER: US/09/986,240
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/243,626
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: SE 0003811-7
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-240-2

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		Query Match	47.4%	Score 337;	DB 10;	Length 132;
		Best Local Similarity	51.2%;	Pred. No. 7.5e-30;		
		Matches	64;	Conservative	20;	Mismatches 41; Indels 0; Gaps 0;
Qy	9	GRRLVDSKGFDEYMKELGVGIALRKKGMAKAPDCIITCDGKNLTIKTSTLKTTQFSGT	68			
		: : : : : : :				
Db	6	GTWKLVDNSKDDYMKSLGVGFATRQVASMTPTTIEKNGDILTLKTHSTFKNTEISFK	65			
Qy	69	LGEKFEEETADGRKTQVCNTDCAALVOHQEWDCKESTITRKLDGKLVCEVMNVTC	128			
		: : : : : : :				
Db	66	LGVEFDDETADRDKVKSVLTLDGGKLVHLOKWGDGETTVLRRELDIGKLLTLTHCTAVCT	125			

QY 129 RYK 133
Db 126 RYK 130

RESULT 6
US-09-901-436A-10
; Sequence 10, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF175D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-10

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Best Local Similarity 51.2%; Pred. No. 7.6e-30;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
QY 9 GRWLVDKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIEKNGDILTLKTHSTFKNTEISFK 66
QY 69 LGKFEETADGRKTQVNFCTDGLVQHOEWGDKESTITRKLDGKLVVCEVMNNVTCT 128
Db 67 LGVEFDETTADDRKVSIVTLVDGGLVHLQKWDGQETTLVRELIDGKLIILTLHTGTAVCT 126
QY 129 RYK 133
Db 127 RYK 131

RESULT 7
US-10-153-740-13
; Sequence 13, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740

FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/734,036
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/307,817
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-153-740-13

Query Match 47.4%; Score 337; DB 12; Length 133;
Best Local Similarity 51.2%; Pred. No. 7.6e-30;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
QY 9 GRWLVDKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIEKNGDILTLKTHSTFKNTEISFK 66
QY 69 LGKFEETADGRKTQVNFCTDGLVQHOEWGDKESTITRKLDGKLVVCEVMNNVTCT 128
Db 67 LGVEFDETTADDRKVSIVTLVDGGLVHLQKWDGQETTLVRELIDGKLIILTLHTGTAVCT 126
QY 129 RYK 133
Db 127 RYK 131

RESULT 8
US-10-153-740-12
; Sequence 12, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>

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; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-740-12

Query Match          46.8%; Score 331; DB 12; Length 133;
Best Local Similarity 47.7%; Pred. No. 3.4e-29;
Matches 62; Conservative 23; Mismatches 45; Indels 0; Gaps 0;

QY 4 VOQLGRLVLVDSKGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKT 63
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Db 2 VDAFVGTKVLVDSKGFDDYMKSLGVGFATRQVGNMTPPTTIEVNGDVTVIKQSTFKNT 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 64 QFSCITLGEFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMN 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 EISFKLVGFEDETTADDRKVKSLVTLDDGGLVHVQKNGQETSILVRMDVGDKLLILTLHG 121
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QY 124 NVTCTRYEK 133
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Db 122 TAVCTRYEK 131
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RESULT 9
US-09-901-436A-7
; Sequence 7, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF175D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-7

Query Match          45.9%; Score 326; DB 10; Length 133;
Best Local Similarity 48.8%; Pred. No. 1.2e-28;
Matches 61; Conservative 25; Mismatches 39; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTPKPTTIEKNGDVTITIKTOSTFKNTINFQ 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 69 LGKFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMNVTCT 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 LGIEFEVTDADDRKVKSLVTLDDGGLVHVQKNGQETTLTRELVDGKLLILTLHGSVST 126
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 129 RYIEK 133
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Db 127 RYIEK 131
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RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
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Db 127 RYIEK 131
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RESULT 10
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/153,740
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-153-740-11

Query Match          45.9%; Score 326; DB 12; Length 133;
Best Local Similarity 48.8%; Pred. No. 1.2e-28;
Matches 61; Conservative 25; Mismatches 39; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
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Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTPKPTTIEKNGDVTITIKTOSTFKNTINFQ 66
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QY 69 LGKFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMNVTCT 128
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Db 67 LGIEFEVTDADDRKVKSLVTLDDGGLVHVQKNGQETTLTRELVDGKLLILTLHGSVST 126
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QY 129 RYIEK 133
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Db 127 RYIEK 131
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RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
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```

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-328

Query Match      30.2%; Score 214.5; DB 9; Length 138;
Best Local Similarity 35.4%; Pred. No. 1.8e-16;
Matches 46; Conservative 36; Mismatches 41; Indels 7; Gaps 4;

QY 9 GRWLVDKSGFDEYMKELGVGIALRK--MGAMAKPDCIITCDGKNLTIKTESTLKTTFQS 66
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 GNMKIIRSENFELLKVLGVNVMRLKIAVAASKPAVEIKQEGDTFYIKTSTIVRTTEIN 65

QY 67 CTLGKFEETADGRKTQTVCNF--TDCALVQHQ---EWDGKESTITRKL-KDGKLVVECV 121
   ||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 FKVGEEFEQTVDRCKSLVKWSENMVMVCEQKLLKGPKTSWPRELTNDGELITLWT 125

QY 122 MNNVCTRIY 131
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Db 126 ADDVVCTRVY 135

RESULT 15
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-848

Query Match      27.4%; Score 195; DB 10; Length 160;
Best Local Similarity 37.7%; Pred. No. 2.9e-14;
Matches 46; Conservative 25; Mismatches 45; Indels 6; Gaps 2;

QY 16 SKGFDEYMKELGVGIALRK--MGAMAKPDCIITCDGKNLTIKTESTLKTTFQSCVLGEKF 73
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Db 36 SENFDELLKALGVNMLRKVAVAASKPHVEIRQDGDQFYIKTSTIVRTTEINFKVGEGF 95
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QY 74 EETTADGRKTQTVCNFTDGCALVQHQ---EWDGKESTITRKLKDGKLVVECVNMYTCTR 129
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 96 EETVDGRKCRSLATWENENKIHCTQTLLLEGDPKTYWTRELANDELILTFGADDDVVCTR 155

QY 130 IY 131
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Db 156 IY 157

Search completed: November 25, 2002, 10:37:10
Job time : 11 secs
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:34:38 ; Search time 15 Seconds
(without alignments)
264.806 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVOOLEGRWRLVDSKGF.....LVCEVMNNVTCTRIYKVE 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	1	US-08-446-600A-4
2	387	54.4	132	1	US-08-409-731A-11
3	387	54.4	132	2	US-08-470-298B-11
4	387	54.4	132	2	US-09-023-073A-11
5	387	54.4	132	4	US-09-361-737-11
6	337	47.4	133	1	US-08-409-731A-10
7	337	47.4	133	2	US-08-470-298B-10
8	337	47.4	133	2	US-08-820-825-13
9	337	47.4	133	2	US-09-023-073A-10
10	337	47.4	133	4	US-09-307-817-13
11	337	47.4	133	4	US-09-361-737-10
12	337	47.4	133	4	US-09-734-036-13
13	331	46.6	133	2	US-08-820-825-12
14	331	46.6	133	4	US-09-307-817-12
15	331	46.6	133	4	US-09-734-036-12
16	326	45.9	131	1	US-08-409-731A-7
17	326	45.9	131	2	US-08-470-298B-7
18	326	45.9	133	2	US-08-820-825-11
19	326	45.9	133	2	US-09-023-073A-7
20	326	45.9	133	4	US-09-307-817-11
21	326	45.9	133	4	US-09-361-737-7
22	326	45.9	133	4	US-09-734-036-11
23	303	42.6	132	4	US-09-043-646-2
24	291.5	41.0	131	2	US-08-820-825-15
25	291.5	41.0	131	4	US-09-307-817-15
26	291.5	41.0	131	4	US-09-734-036-15
27	270	38.0	132	2	US-08-470-298B-12

28	214.5	30.2	138	1	US-08-468-709B-2	Sequence 2, Appli
29	214.5	30.2	138	2	US-08-241-664B-2	Sequence 2, Appli
30	214.5	30.2	138	5	PCT-US93-03936-2	Sequence 2, Appli
31	212	29.8	137	1	US-08-468-709B-4	Sequence 4, Appli
32	212	29.8	137	2	US-08-241-664B-4	Sequence 4, Appli
33	212	29.8	137	5	PCT-US93-03936-4	Sequence 4, Appli
34	210	29.5	137	1	US-08-468-709B-11	Sequence 11, Appl
35	210	29.5	137	2	US-08-241-664B-11	Sequence 11, Appl
36	204.5	28.8	138	1	US-08-468-709B-12	Sequence 12, Appl
37	204.5	28.8	138	2	US-08-241-664B-12	Sequence 12, Appl
38	190.5	26.8	133	1	US-08-554-463-1	Sequence 1, Appli
39	178	25.0	135	1	US-08-409-731A-8	Sequence 8, Appli
40	178	25.0	135	2	US-08-470-298B-8	Sequence 8, Appli
41	178	25.0	135	2	US-08-847-724-4	Sequence 4, Appli
42	174	24.5	135	2	US-08-847-724-6	Sequence 6, Appli
43	174	24.5	135	2	US-09-023-073A-8	Sequence 8, Appli
44	174	24.5	135	3	US-08-899-031-4	Sequence 4, Appli
45	174	24.5	135	4	US-09-361-737-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: NO. 5719126dlund, James J. and Farooqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frost & Jacobs
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
; TELEX: 21-4396 F&J Cin
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; US-08-446-600A-4

Query Match 100.0%; Score 711; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e-79;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATVOOLEGRWRLVDSKGFDEYNKELGVGIALRKMGMAKPDCIITCDGKNLITKTESTL 60

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Db 1 MATVQLEGRWLRVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTL 60
QY 61 KTFQSCITLGEKEEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVEC 120
Db 61 KTFQSCITLGEKEEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVEC 120
QY 121 VMNVVTCRIYKEV 135
Db 121 VMNVVTCRIYKEV 135

RESULT 2
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,731A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PF175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
;
US-08-409-731A-11
Query Match 54.4%; Score 387; DB 1; Length 132;
Best Local Similarity 58.7%; Pred. No. 7.8e-40;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLAKEPTVIISKGGDIITRTSTFKNTEISFK 66

QY 69 LGKEFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVECVMNVVTC 128
Db 67 LGQEFEEETADNRKTKSVITLQSGSLNQVQRWDGKETTIRKLKLVNGKMAECKMKGVVCT 126

QY 129 RIYEKV 134
Db 127 RIYEKV 132

RESULT 3
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
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US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
;
US-08-470-298B-11
Query Match 54.4%; Score 387; DB 2; Length 132;
Best Local Similarity 58.7%; Pred. No. 7.8e-40;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLAKEPTVIISKGGDIITRTSTFKNTEISFK 66

QY 69 LGKEFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVECVMNVVTC 128
Db 67 LGQEFEEETADNRKTKSVITLQSGSLNQVQRWDGKETTIRKLKLVNGKMAECKMKGVVCT 126

QY 129 RIYEKV 134
Db 127 RIYEKV 132

RESULT 4
US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-409-731A-10

Query Match          47.4%; Score 337; DB 1; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGKEFEETTAGRKTQTCVNCFTDQALVQHQEWGDKESTITRKLKDGKLVVECVMMNVVTC 128
Db 67 LGVEFDETTADDRKVKSVITLDGKGLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 7
US-08-470-298B-10
; Sequence 10, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Query Match          47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
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QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGKEFEETTAGRKTQTCVNCFTDQALVQHQEWGDKESTITRKLKDGKLVVECVMMNVVTC 128
Db 67 LGVEFDETTADDRKVKSVITLDGKGLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 8
US-08-820-825-13
; Sequence 13, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-13

Query Match          47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGKEFEETTAGRKTQTCVNCFTDQALVQHQEWGDKESTITRKLKDGKLVVECVMMNVVTC 128
Db 67 LGVEFDETTADDRKVKSVITLDGKGLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131
```



```

RESULT 9
US-09-023-073A-10
; Sequence 10, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-073A-10

Query Match          47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred.No.1.le-33;
Matches    64; Conservative   20; Mismatches   41; Indels      0; Gaps

QY       9 GRWLVDKGFDEYMRELGVGIALRKMGAAPDCIITCDGNLTKTTESTLKTTQFSCT 68
           |::|::::||::|:||:|::|::|::|::|::|::|::|::|::|::|::|:
DB        7 GTWKLVDSKNFDYMKSLGVGFATROVASMKTPTTIENGDIILTLKTHSTFKATEISPK 66
                                           ||
QY       69 LGSEKFETTAGDKRKRTOTVCNFTDGALVQHVGNDKGESTIRKLKDGLVVCEVMNVVTCT 128
           ||::|::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
DB        67 LGSVEFDETADDRKRKSIVTLDGGKLVLHQLKWMDQGETTLLRVLELDIGKLILTHTHGTA VTC 126
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QY       129 RIVEK 133
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DB        127 RTYEK 131

RESULT 10
US-09-307-817-13
; Sequence 13, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-361-737-10

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Best Local Similarity 51.2%; Pred. No. 1.1e-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
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DB 7 GTWKLVDKSNFDDYMKSLGVGFATROVASMTKPTTIIKNGDILTLKTHSTFKNTEISFK 66
QY 69 LGKEFETTTADGRKKTOTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVVECMNNVTCT 128
DB 67 LGVEFETTTADGRKKSIVTLDDGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTA VCT 126
QY 129 RIYEK 133
DB 127 RTYEK 131

RESULT 12
US-09-734-036-13
Sequence 13, Application US/09734036
Patent No. 6413726
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,036
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/307,817
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-734-036-13

Query Match 47.4%; Score 337; DB 4; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.1e-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKGAMAKPDCIITCDGKNLTIKTESTLKTTOFSCT 68
DB 7 GTWKLVDKSNFDDYMKSLGVGFATROVASMTKPTTIIKNGDILTLKTHSTFKNTEISFK 66
QY 69 LGKEFETTTADGRKKTOTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVVECMNNVTCT 128
DB 67 LGVEFETTTADGRKKSIVTLDDGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTA VCT 126
QY 129 RIYEK 133
DB 127 RTYEK 131

RESULT 13
US-08-820-825-12
Sequence 12, Application US/08820825
Patent No. 5945309
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-820-825-12

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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:31:03 ; Search time 36 Seconds
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Title: US-09-788-074-3

Perfect score: 711

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	AA055866	Melanogenic inhibi
2	711	100.0	135	AAU08674	Human keratinocyte
3	699	98.3	158	ABG27577	Novel human diagno
4	689	96.9	135	ABG61772	Novel fatty acid-b
5	624.5	87.8	134	AAU08666	Human NOV10 protei
6	619.5	87.1	163	AAU08665	Human NOV9 protei
7	612	86.1	135	AAU08673	Mouse keratinocyte
8	570.5	80.2	146	ABG60208	Human DITHP polype
9	452.5	63.6	172	AAU10059	Fatty acid-binding
10	430.5	60.5	181	ABG13617	Novel human diagno

11	375	52.7	136	19	AAW40227	Human myelin P2 pr
12	371	52.2	136	19	AAW40228	Bovine myelin P2 p
13	366	51.5	132	21	AAV90320	Human AFABP protei
14	366	51.5	132	23	ABB08076	Human ap2 protein.
15	360	50.6	132	21	AAV90319	Mouse AFABP protei
16	337	47.4	133	22	AAAG66578	Human MDGI polyep
17	332	46.7	131	12	AAAR13559	MDGI active peptid
18	331	46.6	133	22	AAAG66577	Bovine MDGI polyep
19	326	45.9	133	22	AAAG66576	Mouse MDGI polyep
20	322.5	45.4	134	18	AAW31534	Porcine heart-fatt
21	304	42.8	132	16	AAW75423	Mouse cellular x b
22	303	42.6	132	18	AAW22408	Human cytostatin I
23	303	42.6	132	19	AAW80949	Amino acid sequenc
24	303	42.6	132	19	AAW81106	Human cytostatin I
25	303	42.6	132	20	AAW82403	Human cytostatin I
26	297	41.8	117	21	AAAG03847	Human secreted pro
27	291.5	41.0	131	22	AAAG66580	Human cytostatin I
28	291	40.9	132	21	AAAG03957	Human secreted pro
29	269	37.8	522	22	ABG13615	Novel human diagno
30	253.5	35.7	130	22	ABB62690	Drosophila melanog
31	232.5	32.7	117	22	AAU30142	Novel human secret
32	230	32.3	433	22	ABG27578	Novel human diagno
33	223.5	31.4	149	21	AAAB58158	Lung cancer associ
34	215	30.2	132	22	AAU10065	Cytostatin family
35	215	30.2	135	22	AAU10066	Cytostatin family
36	214.5	30.2	138	14	AAAR42211	CRABP-II gene prod
37	214.5	30.2	138	22	AAAB76852	Human lung tumour
38	214.5	30.2	138	23	AAU85507	Clone #19122 of lu
39	212	29.8	137	14	AAAR42212	CRABP-I gene produ
40	200	28.1	88	21	AAAB58740	Breast and ovarian
41	195	27.4	82	22	AAAG75123	Human colon cancer
42	195	27.4	160	21	AAAB43403	Human cancer assoc
43	190.5	26.8	133	16	AAAR75643	Schistosoma manso
44	187.5	26.4	79	22	ABG13616	Novel human diagno
45	174	24.5	219	23	ABP41914	Human ovarian anti

ALIGNMENTS

RESULT 1	
AA055866	
ID	AA055866 standard; Protein; 135 AA.
XX	
AC	AA055866;
XX	
DT	07-DEC-1994 (first entry)
XX	
DE	Melanogenic inhibitor.
XX	
KW	Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;
KW	depigmentation; melanoma.
XX	
OS	Homo sapiens.
XX	
PN	WO9412534-A.
XX	
PD	09-JUN-1994.
XX	
PF	16-NOV-1993; 93WO-US11139.
XX	
PR	24-NOV-1992; 92US-0980513.
PR	01-SEP-1993; 93US-0115172.
XX	
XX	(UYCI-) UNIV CINCINNATI.
XX	
PI	Farooqui JZ, Nordlund JJ;
XX	
DR	WPI; 1994-200198/24.
DR	N-PSDB; AAQ66842.
XX	
PT	Prodn. of a protein for inhibiting melanogenesis - useful for
PT	treating hyper-pigmentary diseases, destroying melanoma cells and

PT for lightening unwanted body hair
 PS Disclosure; Page 5; 40pp; English.
 XX
 CC PCR primers given in AA066843-44 were used to amplify RNA from
 CC human skin previously grafted onto nude mice, thereby providing
 CC DNA (AA066842) encoding melanogenic inhibitor protein (AAR55866).
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 711; DB 15; Length 135;
 Best Local Similarity 100.0%; Pred. No. le-72;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATVOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNTIKTESTL 60
 DB 1 MATVOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNTIKTESTL 60
 QY 61 KTTQFSCITLGERFPEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 DB 61 KTTQFSCITLGERFPEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 QY 121 VMNVVTCRIYEKVE 135
 DB 121 VMNVVTCRIYEKVE 135
 RESULT 2
 AAU08674
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 DT 18-DEC-2001 (first entry)
 XX Human keratinocyte fatty acid binding protein, Mall.
 XX Human; Mal 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antisense therapy.
 XX Homo sapiens.
 OS
 XX WO200160384-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 16-FEB-2001; 2001WO-US05019.
 PF
 XX 17-FEB-2000; 2000US-0183106.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Hotamialigil GS;
 PI
 XX WPI: 2001-570550/64.
 DR
 XX N-PSDB; AAS13247.
 XX
 PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor
 PS Disclosure; Page 2; 27pp; English.
 XX
 CC The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mal1 (keratinocyte
 CC fatty acid binding protein) or Mal1 activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
 CC useful for diagnosing diseases. The present sequence is Human

CC Mal 1.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 711; DB 22; Length 135;
 Best Local Similarity 100.0%; Pred. No. le-72;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATVOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNTIKTESTL 60
 DB 1 MATVOOLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNTIKTESTL 60
 QY 61 KTTQFSCITLGERFPEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 DB 61 KTTQFSCITLGERFPEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 QY 121 VMNVVTCRIYEKVE 135
 DB 121 VMNVVTCRIYEKVE 135
 RESULT 3
 ABG27577
 ID ABG27577 standard; Protein; 158 AA.
 XX
 AC ABG27577;
 DT 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #27568.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI: 2001-639362/73.
 DR
 XX N-PSDB; AAS91764.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX Claim 20; SEQ ID No 57936; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

XX	Homo sapiens.	Db	120 VTNNVTCTRIYKVE 134
OS			
XX			
PN	WO200168851-A2.		
XX			
PD	20-SEP-2001.		
XX			
PF	12-MAR-2001; 2001WO-US07735.		
XX			
PR	10-MAR-2000; 2000US-0188277.		
PR	10-MAR-2000; 2000US-0188316.		
PR	14-MAR-2000; 2000US-0189139.		
PR	14-MAR-2000; 2000US-0189140.		
PR	17-MAR-2000; 2000US-0190231.		
PR	17-MAR-2000; 2000US-0190401.		
XX	(CURA-) CURAGEN CORP.		
PA			
XX	Padigaru M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;		
PI	Majumder K, Li L;		
XX			
DR	WPI: 2001-570869/64.		
DR	N-PSDB; AAS13344.		
XX			
PT	Novel polypeptides and nucleic acids homologous to members of collagen,		
PT	potassium channel, tuftelin family of proteins for diagnosing, treating		
PT	cancer, atherosclerosis, neurological, skin and enamel defect disorders		
PT			
XX			
PS	Claim 1; Page 37; 128pp; English.		
XX			
CC	The invention relates to isolated NOVX (NOVX1-11) polypeptides and		
CC	the polynucleotides that encode them. NOVX polypeptides, polynucleotides		
CC	and anti-NOVX antibodies are useful for treating or preventing a		
CC	pathology associated with NOVX polypeptide in humans and for treating a		
CC	syndrome associated with human disease e.g. disorders characterised by		
CC	altered cell motility, proliferation and migration e.g. cancer,		
CC	angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.		
CC	episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's		
CC	disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,		
CC	asthma, hypertension and seizure (NOV4), enamel defects, such as		
CC	amelogenesis imperfecta and disorders involving enamel defects,		
CC	including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic		
CC	neurological disorders, e.g. paraneoplastic limbic of brain-stem		
CC	encephalitis occurring during testicular cancer, diabetes, reproductive		
CC	health, metabolic and endocrine disorders, gastrointestinal disorders,		
CC	immune disorders and autoimmune diseases, respiratory disorders, bone		
CC	disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell		
CC	growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and		
CC	atherosclerosis, abdominal aortic aneurysm and neurological disorders		
CC	(NOV11). NOVX polypeptide is also useful for identifying an agent that		
CC	binds to it and a cell expressing NOVX polypeptide is useful for		
CC	identifying a therapeutic agent for use in treatment of a NOVX related		
CC	pathology. The antibodies and a polypeptide having 95% sequence identity		
CC	to NOVX polypeptide are useful for treating a pathological state in a		
CC	mammal. The present sequence represents NOV10, a possible epidermal		
CC	fatty acid-binding protein family member.		
XX			
SQ	Sequence 134 AA;		
	Query Match 87.8%; Score 624.5; DB 22; Length 134;		
	Best Local Similarity 88.9%; Pred. No. 6.7e-63;		
	Matches 120; Conservative 5; Mismatches 9; Indels 1; Gaps 1;		
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DB	1 MATVQQLGRRWLVDSSKGFDEYNKELGVGIALRKKMGAMAKPCIIITCDGKNLTIKTESTL 60		
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QY	121. VMNNVTCTRIYKVE 135		

[illegible]

Db	97	STLKSYSFLTLRGKFRCTTGGRRKTQT-CFTTGTTLVRHOKWNGCKEKI-RKLKDRKLIV	154
Qy	118	VECVNMNVTCRIYKEV	135
		(:>::: :	
Db	155	VDCIINNVTCTQIYKEV	172
RESULT 10			
ABG13617	ID	ABG13617 standard; Protein; 181 AA.	
XX	XX		
AC	AC	ABG13617;	
XX	XX		
DT	18-FEB-2002	(first entry)	
XX	XX		
XX	XX	Novel human diagnostic protein #13608.	
XX	XX		
KW	Human;	chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement;	medical imaging; diagnostic; genetic disorder.	
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO200175067-A2.		
XX	XX		
PD	11-OCT-2001.		
XX	XX		
PF	30-MAR-2001; 2001WO-US08631.		
XX	XX		
PR	31-MAR-2000; 2000US-0540217.		
XX	XX		
PR	23-AUG-2000; 2000US-0649167.		
XX	XX		
PA	(HYSE-) HYSEQ INC.		
XX	XX		
PI	Drmanac RT, Liu C, Tang YT;		
XX	XX		
DR	WPI: 2001-639362/73.		
DR	N-PSDB: AAS77804.		
XX	XX		
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity		
XX	XX		
PS	Claim 20; SEQ ID NO 43976; 103pp; English.		
XX	XX		
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used, in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. ABG00010-ABG30377 represent novel human		
CC	diagnostic amino acid sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences .		
XX	XX		
SQ	Sequence	181 AA;	
Query Match			
Best Local Similarity 60.5%; Score 430.5; DB 22; Length 181;			
Matches 99; Conservative 72.3%; Pred. No. 1.le-40;			
Matches 9; Gaps 10; Mismatches 19; Indels 9; Gaps 9;			

Db 67 LGQEFETTADNRKTSIVTLQSGSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 126
 QY 129 RIVE 132
 Db 127 RIVD 130

RESULT 12
 AAW40228
 ID AAW40228 standard; Protein; 136 AA.

XX AC AAW40228;
 XX DT 26-JUN-1998 (first entry)
 XX DE Bovine myelin P2 protein.
 XX KW Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
 KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
 KW gammopathy.
 XX OS Bos taurus.
 XX PN WO9803647-A2.
 XX PD 29-JAN-1998.
 XX PF 18-JUL-1997; 97WO-DE01535.
 XX PR 18-JUL-1996; 96DE-1029095.
 XX PA (GOLD/) GOLD R.
 PA (WEIS/) WEISHAAPT A.
 XX PI Gold R, Weishaupt A;
 PI WPI; 1998-120772/11.

XX Recombinant myelin proteins for treating T-cell mediated disease of
 PT peripheral nervous system - by high dose antigen therapy, causing
 PT apoptosis in T cells, for treating e.g. polyneuritis or
 PT Guillain-Barre syndrome
 XX Disclosure; Fig 4; 14pp; German.
 PS The present sequence is the bovine myelin P2 protein, which can
 CC be used to treat T-cell mediated diseases of the peripheral nervous
 CC system, especially chronic-inflammatory polyneuritis,
 CC Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
 CC of gammopathy.
 XX SQ Sequence 136 AA;

Query Match 52.2%; Score 371; DB 19; Length 136;
 Best Local Similarity 57.3%; Pred. NO. 4.2e-34;
 Matches 71; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 9 GWRRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
 Db 7 GTWKLVSSENFDDYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 66
 QY 69 LGQEFETTADNRKTSIVTLQSGSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 128
 Db 67 LGQEFETTADNRKTSIVTLQSGSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 126
 QY 129 RIVE 132
 Db 127 RIVD 130

RESULT 13
 AAY90320

ID AAY90320 standard; Protein; 132 AA.
 AC AAY90320;
 XX DT 22-NOV-2000 (first entry)
 XX DE Human AFABP protein sequence.
 XX KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
 KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
 KW serum cholesterol; therapy; human.
 XX OS Homo sapiens.
 XX PN WO2000047734-A1.
 XX PD 17-AUG-2000.
 XX PF 11-FEB-2000; 2000WO-US03560.
 XX PR 12-FEB-1999; 99US-0119880.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Lee M, Perrella MA, Hotamisligil GS;
 XX WPI; 2000-506094/45.
 XX N-PSDB; AAA37717.
 XX Reducing expression of adipocyte fatty acid binding protein through
 PT administration of a compound is used to inhibit formation of an
 PT atherosclerotic lesion -
 XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the human AFABP (adipocyte fatty
 CC acid binding protein) protein sequence. The invention relates to a method
 CC for inhibiting formation of an atherosclerotic lesion comprising
 CC administering to a mammal a compound that reduces expression of adipocyte
 CC fatty acid binding protein (AFABP). The method is used to inhibit
 CC formation of atherosclerotic lesions. The method is used to identify
 CC compounds which can be used to inhibit formation of atherosclerotic
 CC lesions through inhibition of AFABP binding to an intracellular ligand
 CC in a macrophage or adipocyte, inhibition of development of an
 CC atherosclerotic lesion, inhibition of a macrophage differentiating into
 CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity
 CC may be inhibited to treat atherosclerosis or to treat individuals at risk
 CC of developing atherosclerosis. Inhibiting AFABP expression or activity
 CC reduces the development of atherosclerotic lesions despite a high level
 CC of serum cholesterol.

SQ Sequence 132 AA;
 Query Match 51.5%; Score 366; DB 21; Length 132;
 Best Local Similarity 55.2%; Pred. NO. 1.5e-33;
 Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 9 GWRRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
 Db 7 GTWKLVSSENFDDYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 66
 QY 69 LGQEFETTADNRKTSIVTLQSGSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 128
 Db 67 LGQEFETTADNRKTSIVTLQSGSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 126
 QY 129 RIVE 133
 Db 127 RIVER 131
 RESULT 14
 ABB08076
 ID ABB08076 standard; protein; 132 AA.

```

XX AC ABB08076;
XX DT 10-SEP-2002 (first entry)
XX DE
XX KW Human ap2 protein.
XX KW ap2; antiarteriosclerotic; cardiant; cerebroprotective; antianginal;
XX KW cytosolic protein; adipocyte; HMG CoA reductase; pravastatin; human.
XX OS Homo sapiens.
XX PN US2002035064-A1.
XX PD 21-MAR-2002.
XX PF 13-JUL-2001; 2001US-0905235.
XX PR 17-SEP-1998; 98US-100677P.
XX PR 07-SEP-1999; 99US-0390275.
XX PA (ROBL/) ROBL J A.
XX PA (PARK/) PARKER R A.
XX PA (BILL/) BILLER S A.
XX PA (JAMI/) JAMIL H.
XX PA (JACO/) JACOBSON B L.
XX PA (KODU/) KODUKULA K.
XX PI Robl JA, Parker RA, Biller SA, Jamil H, Jacobson BL, Kodukula K;
XX WPI: 2002-470589/50.
XX
XX PT Method useful for treatment of e.g. atherosclerosis, myocardial
XX PT infarction, angina involves administering ap2 inhibitor e.g.
XX PT (2'-(4,5-diphenyl-oxazol-2-yl)-biphenyl-3-yloxy)-acetic acid -
XX PS Disclosure; Page 16; 26pp; English.
XX
XX CC The invention relates to the treatment of atherosclerosis which involves
XX CC administering an ap2 inhibitor or a combination of an ap2 inhibitor and
XX CC another type antiatherosclerotic agent, for example, an HMG CoA reductase
XX CC inhibitor such as pravastatin. The method is used for treating
XX CC atherosclerosis; for preventing, inhibiting or reducing risk of
XX CC cardiovascular disorders e.g. cardiac and/or cerebral ischaemia,
XX CC myocardial infarction, angina, peripheral vascular disease and stroke.
XX CC The present sequence represents the amino acid sequence of human ap2
XX CC protein, a cytosolic protein present in adipocytes.
XX SQ Sequence 132 AA;
    Query Match 51.5%; Score 366; DB 23; Length 132;
    Best Local Similarity 55.2%; Pred. No. 1.5e-33;
    Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
    QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
    DB 7 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVIITKSESTFKNTEISFI 66
    QY 69 LGKEFETTTADGRKTQTCVNCFTDGLVHOEWDPGKESTITRKLKDGKLVVCEVMNNVTCT 128
    DB 67 LGQFEDEVTTADRRKVKSTITLDGGVLVHVQKWDGKSTTTIKRRKREDKLVVCEVMKGVST 126
    QY 129 RYIEK 133
    DB 127 RYVER 131
    RESULT 15
    ID. AAY90319
    XX ID. AAY90319 standard; Protein; 132 AA.
    AC AAY90319;
    XX

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DT 22-NOV-2000 (first entry)
XX Mouse AFABP protein sequence.
XX AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
XX KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
XX KW serum cholesterol; therapy; mouse.
XX OS Mus sp.
XX WO200047734-A1.
XX PN 17-AUG-2000.
XX PD 11-FEB-2000; 2000WO-US03560.
XX PR 12-FEB-1999; 99US-0119880.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lee M, Perrella MA, Hotamisligil GS;
XX WPI: 2000-506094/45.
XX N-PSDB; AAA37716.
XX
XX PT Reducing expression of adipocyte fatty acid binding protein through
XX PT administration of a compound is used to inhibit formation of an
XX PT atherosclerotic lesion -
XX PS Disclosure; Page 14; 43pp; English.
XX
XX CC This sequence represents the mouse AFABP (adipocyte fatty
XX CC acid binding protein) protein sequence. The invention relates to a method
XX CC for inhibiting formation of an atherosclerotic lesion comprising
XX CC administering to a mammal a compound that reduces expression of adipocyte
XX CC fatty acid binding protein (AFABP). The method is used to inhibit
XX CC formation of atherosclerotic lesions. The method is used to identify
XX CC compounds which can be used to inhibit formation of atherosclerotic
XX CC lesions through inhibition of AFABP binding to an intracellular ligand
XX CC in a macrophage or adipocyte, inhibition of development of an
XX CC atherosclerotic lesion, inhibition of a macrophage differentiating into
XX CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity
XX CC may be inhibited to treat atherosclerosis or to treat individuals at risk
XX CC of developing atherosclerosis. Inhibiting AFABP expression or activity
XX CC reduces the development of atherosclerotic lesions despite a high level
XX CC of serum cholesterol.
XX SQ Sequence 132 AA;
    Query Match 50.6%; Score 360; DB 21; Length 132;
    Best Local Similarity 55.2%; Pred. No. 7.2e-33;
    Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
    QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
    DB 7 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVIITKSESTFKNTEISFK 66
    QY 69 LGKEFETTTADGRKTQTCVNCFTDGLVHOEWDPGKESTITRKLKDGKLVVCEVMNNVTCT 128
    DB 67 LGVEFEDEVTTADRRKVKSTITLDGGALVQVQKWDGKSTTTIKRRKRDGKLVVCEVMKGVST 126
    QY 129 RYIEK 133
    DB 127 RYVER 131
    Search completed: November 25, 2002, 10:35:11
    Job time : 37 secs

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GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:24:47 ; Search time 87.5 Seconds
(without alignments)
6023.640 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 2239
Sequence: 1 aatggaggaacatctagc.....tctatgagaagtgcattga 1279

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q/cgn2_1/USPTO.spool/US09788074/runat_25112002_093514_15675/app_query.fasta_1.1415
-DB-SPTREMBL_21 -ONFT-fastan -SUFFIX-rspt -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09788074.ecgn_1.124.erunat_25112002_093514_15675 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	183.5	8.2	132 13 Q90X55	Q90x55 gallus gall

2	180	8.0	132 13 Q90W92	Q90w92 fundulus he
3	179.5	8.0	113 6 Q9XSG4	Q9xsg4 oryctolagus
4	176.5	7.9	99 6 Q97675	Q97675 sus scrofa
5	171.5	7.7	132 13 Q8QHA8	Q8qha8 anser anser
6	169.5	7.6	86 13 Q8UWD3	Q8uwd3 anser anser
7	168.5	7.5	132 11 Q9DAK4	Q9dak4 mus musculus
8	165.5	7.4	125 6 Q9XSI5	Q9xsi5 equus caball
9	160.5	7.2	111 13 Q90ZG6	Q90zg6 brachydanio
10	159.5	7.1	166 4 Q9H047	Q9h047 homo sapien
11	157.5	7.0	97 11 Q9QV90	Q9qv90 mus sp. lng
12	155	6.9	53 13 Q9QW19	Q9qw19 gallus gall
13	155	6.9	134 13 Q97663	Q97663 gobionototh
14	154.5	6.9	132 13 Q918N9	Q918n9 brachydanio
15	152	6.8	134 13 Q97663	Q97663 notiothenia
16	152	6.8	134 13 Q97691	Q97691 cryodraco a
17	151.5	6.8	133 13 Q8UWG7	Q8uwg7 brachydanio
18	151.5	6.8	150 11 Q9R290	Q9r290 rattus norv
19	150	6.7	134 13 Q97666	Q97666 paraeaeic
20	148	6.6	135 13 Q91896	Q91896 anguilla ja
21	147	6.6	133 13 Q97669	Q97669 notiothenia
22	146	6.5	133 13 Q97667	Q97667 chaenoceph
23	146	6.5	133 13 Q97668	Q97668 cryodraco a
24	146	6.5	133 13 Q97670	Q97670 gobionototh
25	143.5	6.4	136 5 Q8WR15	Q8wr15 metapeneus
26	138.5	6.2	132 11 Q9DAL2	Q9dal2 mus musculu
27	138	6.2	100 13 Q97664	Q97664 rhigophila
28	137	6.1	132 5 Q9UIG6	Q9uig6 fasciola he
29	126	5.6	136 5 Q91814	Q91814 caenorhabdi
30	125	5.6	114 11 Q99M00	Q99m00 mus musculu
31	124	5.5	114 11 Q9VGM2	Q9vgm2 drosophila
32	117	5.2	133 5 Q9BWK1	Q9bmk1 echinococcu
33	117	5.2	133 5 Q9BLY5	Q9bly5 echinococcu
34	117	5.2	133 5 Q967X3	Q967x3 echinococcu
35	114	5.1	135 5 Q91812	Q91812 caenorhabdi
36	113	5.0	147 13 Q9PSA5	Q9psa5 xenopus lae
37	112	5.0	132 5 Q45035	Q45035 schistosoma
38	110	4.9	132 5 Q9BME8	Q9bme8 schistosoma
39	110	4.9	132 5 Q26517	Q26517 schistosoma
40	109	4.9	98 5 Q8T5U8	Q8t5u8 schistosoma
41	109	4.9	132 5 Q61236	Q61236 manduca sex
42	109	4.9	133 5 Q8T5U9	Q8t5u9 schistosoma
43	108	4.8	128 13 Q919A9	Q919a9 lygodactylu
44	103	4.6	126 5 Q94567	Q94567 fasciola g1
45	103	4.6	132 5 Q9UAS2	Q9uas2 fasciola g1

ALIGNMENTS

RESULT 1

Q90X55 PRELIMINARY; PRT; 132 AA.
ID AC Q90X55; Q90X56;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Adipocyte fatty acid binding protein.
GN AFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Study on chicken AFABP gene as candidate gene for fatness trait.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

```
RT in chicken.*;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene
in chicken.*;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF432507; AAL30744.2; -
DR EMBL: AF432506; AAL30743.1; -
DR InterPro: IPR000463; Fatty_acid_BP
DR InterPro: IPR000566; Lipocin_cyFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PROSITE: PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14894 MW; 4f5905FAB8DA268B CRC64;

Alignment Scores:
Pred. No.: 5.41e-12 Length: 132
Score: 183.50 Matches: 51
Percent Similarity: 33.17% Conservative: 16
Best Local Similarity: 25.25% Mismatches: 25
Query Match: 8.20% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q90X55 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCGCAGACTGCTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 44
QY 191 TGTGATGGCAACACATCACGGTCAAAACCGAGACGACACTGAAGCAGCTGTGTTCTCT 250
Db 45 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGATTGTGATGAACACACAGCTGATGGCAAGAAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyGluGluPheAspGluThrThrAlaAspArgLysThr-LysAsn-- 83
QY 311 TACAACATACCTGTGTGAAGCGACAGAACTTCTAGATTTACAGATTAATAATGCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCATAGTTGTATTGTGAACAAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
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QY 551 CGAAGACTTGTGGAGTGGTGGGTCTGGGGTTCCTTCACTTTGGAAGATCATGAAC 610
Db 83 ----- 83
QY 611 TAACACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGCGGTGCCCTGTCTCAGCA 670
Db 84 -----ValIleThrLeuAspSerGlyThrLeuLysGlnVa 95
QY 671 CCAGCAATGGGAGGAGGACGACGATCAACAAAGGATGCGGAGGAGGATGAT 730
Db 95 lGlnLysTrpAspGlyLysGluThrValIleLysArgLysValValAspGlyAsnLeuLe 115
QY 731 CGTG 734
Db 115 uVal 116
RESULT 2
Q90W92
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Db	76	-----	76
Qy	551	CGAAGACTGTGTTGGAGTGGTGCTGGGTCCTTCACTTTTGAAGATGATGAAC	610
Db	76	-----	76
Qy	611	TAACTACCCTGTATTFTTTGCAGAGCGTCTCACACTTCCAAAGACGGTCCCTCGTGTCCAGCA	670
Db	77	-----	78
Qy	671	CCACCATGGGACGGGAAGAGACGACGATACAAGAANAACCTGAAGATGGGGAAGATGAT	730
Db	'88	IglnLysTrpAspGlyLysSerThrThrIleLysArgLysArgGluGlyAspLysLeuVa	108
Qy	731	CGTG 734	
Db	108	Ival 109	
RESULT 4			
ID	O97675	PRELIMINARY;	PRT; 99 AA.
AC	O97675;		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	Adipocyte fatty acid binding protein (Fragment).		
CN	AP2.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99410873; PubMed=10481259;		
RA	Ding S.T., McNeel R.L., Mersmann H.J.;		
RT	"Expression of porcine adipocyte transcripts: tissue distribution and differentiation in vitro and in vivo.";		
RL	Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 123:307-318(1999).		
DR	EWBL; AF102872; AAC78684.1; "		
DR	HSSP; P04117; ILLD.		
DR	InterPro; IPR000463; Fatty_acid_BP.		
DR	InterPro; IPR000566; Lipocln_cytFABP.		
DR	Pfam; PF00061; lipocalin; 1.		
DR	PRINTS; PR00178; FATTVACIDBP.		
FT	NON_TER 1		
FT	NON_TER 99		
SO	SEQUENCE 99 AA; 10804 MW; CIE053304FB18F3E CRC64;		
Alignment Scores:			
Pred. No.:	3-23e-11	Length:	99
Score:	176.50	Matches:	49
Percent Similarity:	33.00%	Conservative:	17
Best Local Similarity:	24.50%	Mismatches:	24
Query Match:	7.88%	Indels:	110
DB:	6	Gaps:	1
US-09-788-074-2 (1-1279) x O97675 (1-99)			
Qy	137	GGACTGGCTCTTAGGAAGATGGTGCCATGCCAACGCCAGCTGTATCATTACGTGTGAT	196
Db	1	GlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnLeutlleIleThrValAsn	20
Qy	197	GGCAACACATCATCGGTCAAACCCGACGACACAGTGAAGACGACTGTGTTCTTGTAAAC	256
Db	21	GlyaspMetIleThrIleArgSerGluserTherPhelyAsnThrGluIleAlaPheLys	40
Qy	257	CTGGGAGAGAAGTTTGATGAACACACAGCTGATGGCAGAAAACCTGAGGTGACGCTACAAC	316
Db	41	LeuGlyGlnGluPheaspGluValThrAlaaspasparg-Lysvallysser-----	57
Qy	317	ATACTGTGAAGCGACGAAGCTCTAGATTTCACAGATTAAATTCGATTAAACAATGTCTGT	370

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Db 57 ----- 57
QY 377 ACTTACTGCAAGGCTGACTGATAAACTACTTTATGAGTTGACTTTTGATAAATTAG 436
Db 57 ----- 57
QY 437 TAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAGCACAT 496
Db 57 ----- 57
QY 497 AGTTGTATTGTGACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGCGCAAGA 556
Db 57 ----- 57
QY 557 CTGTGTTGGAGTGTGTGGTCTCTGGGGTTCCTTACCTTTTGAAGATGATGAACATACTA 616
Db 57 ----- 57
QY 617 CCTGTATTTTTCAGACGCTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCACCAAGCA 676
Db 58 -----ThrlleThrLeuAspGlyAlaLeuValGlnValGlnLy 71
QY 677 ATGGGACGGGAAGCAGCAGCATACACAGAAACTGAAGGATGGGAAGATGATCGTG 734
Db 71 strPaspGlyLysThrThrIleAsnArgLysIleValAlaAspAspLysLeuValVal 90
RESULT 5
Q8QHA8 PRELIMINARY; PRT; 132 AA.
AC Q8QHA8;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Adipocyte fatty acid-binding protein.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Ao J., Wang Q., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid-binding protein gene
in goose.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF479610; AAL79836.1;
SQ SEQUENCE 132 AA; 14772 MW; 5FD4817B02DA31BB CRC64;

Alignment Scores:
Pred. No.: 1.32e-10 Length: 132
Score: 171.50 Matches: 50
Percent Similarity: 33.17% Conservative: 17
Best Local Similarity: 24.75% Mismatches: 25
Query Match: 7.66% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q8QHA8 (1-132)
QY 131 GGAGTAGGACTGCTTATAGGAAGATGGCTGCATGGCAAGCAGACTGTATCATTCAGC 190
Db 25 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 44
QY 191 TGTGATGGCAACAACATACGCTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCTCT 250
Db 45 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTGCGCAAGAAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyGluGluPheAspGluThrThrAlaAspAspArgLysThr-LysAsn-- 83
QY 311 TACAACATACTGTGAAGCCAGACAGACTTCTAGATTACAGATTAAATTGCATTACAAAT 370
Db 83 ----- 83

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QY 371 GTCTGTACTTACTGCTCAAGGCTGACTGATAAACTACTTTATGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATGTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACACCCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGTCCAGCA 670
Db 84 -----ValIleThrLeuAspSerGlyAlaLeuLysGlnVa 95
QY 671 CCAGCAATCGGACGGAAGGAGAGACGATACACAGAAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnLysGlyAspGlyLysGluThrValIleLysArgArgValValAlaAspGlyAsnLeuLe 115
QY 731 CGTG 734
Db 115 uVal 116
RESULT 6
Q8UWD3 PRELIMINARY; PRT; 86 AA.
AC Q8UWD3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Adipocyte fatty acid binding protein (Fragment).
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Ao J., Wang Q., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene
in goose.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442493; AAL35352.1;
DR InterPro; IPR000566; Lipoclin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9560 MW; 44789073854EF6C8 CRC64;

Alignment Scores:
Pred. No.: 2.01e-10 Length: 86
Score: 169.50 Matches: 49
Percent Similarity: 33.16% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 21
Query Match: 7.57% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q8UWD3 (1-86)
QY 134 GTAGGACTGCTTCTAGGAAGATGGCTGCATGGCAAGCAGACTGTATCATTCAGTGT 193
Db 1 ValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnValThrIleSerIle 20
QY 194 GATGCCAACAAACATCAGCGTCAAAACCGAGACGACAGTGAAGACGACTGTGTCTCTGT 253
Db 21 AsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSerPhe 40
QY 254 AACCTGGGAGAGAAGTTTGTGATAACGACAGCTGTGCGCAAGAAACTGAGGTCAGCTAC 313

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Db 41  LysLeuGlyGluGluPheAspGluThrThrAlaAspArgLysThr-LysAsn----- 58
QY 314 AACATACTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAAATTCGATTAAACAATGTC 373
Db 58 ----- 58
QY 374 TGTACTTACTGCCAAGGGTGTGACTGAAAAAACACTTATTTATGGAGTTGACTTTTGATAAAT 433
Db 58 ----- 58
QY 434 TAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTATCAGTTTCTAGATCGAAAAGCA 493
Db 58 ----- 58
QY 494 CATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGCGCA 553
Db 58 ----- 58
QY 554 AGACTTGTGGAGTGGTGTGGGTCCCTGGGGTTCCTTCACTTTGGAGATGATGAACATA 613
Db 58 ----- 58
QY 614 CTACCCTGTATTTTTCAGACGCTGTCACCTTCCAGACGGTCCCTGTGTCAGCACCA 673
Db - 59 -----ValleThrLeuGluAsnGlySerLeuLysGlnValG1 71
QY 674 GCAATGGGCGGAGGAGACGACGATACAAAGAAAACACTGAAGGAT 719
Db 71 nLysTTrpAspGlyLysGluThrIleLeuLysArgLysValValAsp 86
RESULT 7
Q9DAK4 PRELIMINARY; PRT; 132 AA.
ID Q9DAK4
AC Q9DAK4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1700008G05RIK protein.
GN 1700008G05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005765; BAB24227.1; -.
DR HSSP; P02690; 1PMP.
DR MGD; MGI:1922747; 1700008G05RIK.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocin_cytFABP.
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DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 132 AA; 14758 MW; 7A20C53780845F61 CRC64;
Alignment Scores:
Pred. No.: 2,94e-10 Length: 132
Score: 168.50 Matches: 51
Percent Similarity: 32.84% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 27
Query Match: 7.53% Indels: 110
DB: 11 Gaps: 2
US-09-788-074-2 (1-1279) x Q9DAK4 (1-132)
QY 131 GGATAGGACTGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyArgAlaSerArgLysLeuGlyCysLeuAlaLysProThrValThrIleSer 44
QY 191 TGTGATGGCAACAACATCAGCGGTCAAAACCGAGAGACAGTGAAGAGGACTGTGTCTCT 250
Db 45 ThrAspGlyAspLeuIleThrIleLysThrLysSerIlePheLysAsnLysGluIleSer 64
QY 251 TGTAACTGGGACAGAAAGTTTGTATGAAACGACAGCTGATGGCAGAAAACTGAGGTGAGC 310
Db 65 PheLysLeuGlyGluGluPheGluThrThrProSerGlyArgLysSer-LysSerTh 84
QY 311 TACAACATACTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAAATTCATTAACAAT 370
Db 84 r----- 84
QY 371 GTCTGTACTTACTGCCAAGGGTGTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 84 ----- 84
QY 431 AATTAGTAAGTCCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 84 ----- 84
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 85 -----ValleLeu----- 87
QY 551 CGAAGACTTGTTCGGAGTGGTGGTCCCTGGGGGTTCCTTCACTTTGGAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAGACGGTCCCTGGTGCAGCA 670
Db 88 -----AspAsnAspSerLeuValGlnVa 95
QY 671 CCAGCAATGGGCGGGAAGGAGAGACGACGATACAGAAAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnAspTrpAspGlyLysGluAlaThrIleCysArgArgLeuValAspGlyLysMetVa 115
QY 731 CGTGGTGCAGC 740
Db 115 lValGluSer 118
RESULT 8
Q9XS15 PRELIMINARY; PRT; 125 AA.
ID Q9XS15;
AC Q9XS15;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Heart-type fatty acid-binding protein (Fragment).
GN FABP3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
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RA Schaap F.G., Pelsers M.M.A.L., van der Vusse G.J., Glatz J.F.C.;
RT "Cloning of equine H-FABP cDNA.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143950; AAD32219.1; -.
DR HSSP: P10790; 1BWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000586; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;

Alignment Scores:
Pred. No.: 6.45e-10 Length: 125
Score: 165.50 Matches: 48
Percent Similarity: 32.18% Conservative: 17
Best Local Similarity: 23.76% Mismatches: 27
Query Match: 7.39% Indels: 110
DB: 6 Gaps: 1

US-09-788-074-2 (1-1279) x Q9XSI5 (1-125)
QY 131 GGAGTAGGACTGCTCTTAGGAGATGGTCCATGCCCAAGCCAGACTGTATCATACG 190
Db 17 GlyValGlyPheAlaThrArgGlnValAlaAsnMetThrLysProThrThrIleIleGlu 36
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGACGACGACGATGAAGACGCTGTCTCT 250
Db 37 ValAsnGlyAspThrIleThrIleLysThrHisSerThrPhelLysAsnThrGluIleSer 56
QY 251 TGTAACTGTGGAGAGAGTTGTATGAACGACACAGCTGTGGCAGAAAACTGAGTCAGC 310
Db 57 PhelLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 75
QY 311 TACAACATACTGTGAGCGACAGACAGCTTCTAGATTTCAGATTAAATTGCATTACAAT 370
Db 75 ----- 75
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 75 ----- 75
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTCTTAGATCGAAAA 490
Db 75 ----- 75
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGGTGGAGTTCAGAGAGGAAAGG 550
Db 75 ----- 75
QY 551 CGAAGACTTGTGGAGTGGTGGTCCCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 75 ----- 75
QY 611 TAACACTACCTGTATTTTTCAGACGGTCTCCACCTTCCAAAGAGGGTCCCTGGTCCAGCA 670
Db 76 -----LeuValThrLeuAspGlyGlyLysLeuValHisVa 87
QY 671 CCAGCAATGGGCGGAGGAGACGACGATACAAAGAACTCAAGCATGGGAGATGAT 730
Db 87 lGlnGluTrpAsnGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI1 107
QY 731 CGTG 734
Db 107 eLeu 108

RESULT 9
Q90ZG6 PRELIMINARY; PRT; 111 AA.
AC Q90ZG6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
BT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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DE D168 protein (Fragment).
GN D168.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
RT "A systematic search for the downstream target genes of the midbrain-
RT MHB reciprocal inductive signaling by ordered differential display
RT revealed the expression of ephrin-A3 in the posterior tectum of
RT zebrafish embryos.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB055675; BAB62806.1; -.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
FT NON_TER 1
SQ SEQUENCE 111 AA; 12444 MW; 82EDA23FDAAB5A8 CRC64;

Alignment Scores:
Pred. No.: 2.37e-09 Length: 111
Score: 160.50 Matches: 47
Percent Similarity: 34.31% Conservative: 23
Best Local Similarity: 23.04% Mismatches: 24
Query Match: 7.17% Indels: 110
DB: 13 Gaps: 3

US-09-788-074-2 (1-1279) x Q90ZG6 (1-111)
QY 125 CCCACAGGAGTAGGACTGGCTCTTAGGAAGATGGTCCATGCCCAAGCCAGACTGTATC 184
Db 2 ProLeuGlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrIleVal 21
QY 185 ATTACCTGTGATGGCAACACATCAGCGTCAAAACCGACGACGACGATGAAGACGACTGTG 244
Db 22 IleSerHisGluGlyAspLysValIleLysThrLeuSerThrPhelLysAsnThrGlu 41
QY 245 TTCTCTTTAACTGGGAGAGAGTTGTATGAACACACAGCTGTATGCCAGAAAACTGAG 304
Db 42 IleSerPhelLysLeuGlyGluPheAspGluThrThrAlaAspArg-HisVally 61
QY 305 GTCAGCTACAACATACTGTGAAGCGACAGAGCTTCTAGATTTCAGATTAAATTGCATT 364
Db 61 SSe----- 62
QY 365 AACAACTGTCTGACTTACTTGCCTCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACT 424
Db 63 -ThrValSerLeu----- 66
QY 425 TTGCATAAAATTAGTAAAGTCCCGAGGACTAAGAAATCAAGACATCTTATGAGTTTCTAGAT 484
Db 66 ----- 66
QY 485 CGAAAAGCACATAGTTGTTATTGTGGAACAAATACAGTATGATGGGGTGGAGTTCAGAGAGG 544
Db 66 ----- 66
QY 545 GAAAGCGAAGACTTGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 604
Db 67 -GluGlyAspAsn----- 70
QY 605 ATGAACTAACTACCTGTTATTTTTCAGAGAGGCTCTGCACCTTCCCAAGACGGTCCCTGGT 664
Db 71 -----LeuVa 72
QY 665 CCAGCACACAGCAATGGACGGGAAGGAGAGACGACGATAACAGAAAACTGAAGATGGGAA 724
Db 72 lGlnValGlnArgTrpAspGlyLysGluThrLysPheValArgGluIleLysAspGlyly 92
QY 725 GATGATCGTG 734
Db 725 -----
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Db 92 smetValMet 95
RESULT 10
Q9H047
ID Q9H047 PRELIMINARY; PRT; 166 AA.
AC Q9H047;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE Hypothetical 18.8 kDa protein.
GN DKF2P547J2313.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDJB databases.
DR EMBL; AL512688; CAC21646.1; -.
DR HSSP; P10790; LBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 18829 MW; 4E88C1139530F07A CRC64;

Alignment Scores:
Pred. No.: 3.44e-09 Length: 166
Score: 159.50 Matches: 50
Percent Similarity: 33.17% Conservative: 18
Best Local Similarity: 24.39% Mismatches: 25
Query Match: 7.12% Indels: 112
DB: 4 Gaps: 4

US-09-788-074-2 (1-1279) x Q9H047 (1-166)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleLeuSer 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 45 GlnGluGlyAspLysValValIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACAGCAGCTGTATGCGGAGAAACACTGAGGTCAGC 310
Db 65 PheGlnLeuGlyGluPheAspGluThrThrAlaAspArg 79
QY 311 TACAACATCTGTGGAAGCGACAGACGCTTCTAGATTTACAGATTAAATTTGCATTAACAAT 370
Db 80 -----AsnCys----- 81
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGCGAGTTGACTTTTGATA 430
Db 81 ----- 81
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 82 -----Lys 82
QY 491 GCACATAGTTGTTATGTAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 83 Ser-ValValSerLeu----- 87
QY 551 CGAAGACTGTTGGAGTGCTGGGTGCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTCCAAGCGGT---GCCCTGGTCCA 667

Db 88 -----||||| |||||
QY 668 GCACCAGCAATGGGAGCGGAGGAGCAGACGATACACAGAACTGAAGATGGGAAGAT 727
Db 94 stleGlnLysTrpAspGlyLysGluThrAsnPheValArgGluIleLysAspGlyLysMe 114
QY 728 GATCGTGGTGAGC 740
Db 114 tValMetValSer 118

RESULT 11
Q9QV90
ID Q9QV90 PRELIMINARY; PRT; 97 AA.
AC Q9QV90;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE LMG-14-FATTY acid-binding protein (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
[1]
RP SEQUENCE.
RX MEDLINE=93191717; PubMed=8447836;
RA Bansal M.P., Medina D.;
RT "Expression of fatty acid-binding proteins in the developing mouse
mammary gland.";
RL Biochem. Biophys. Res. Commun. 191:61-69(1993).
DR HSSP; P10790; LBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 10752 MW; 35CE0EEEC2004245 CRC64;

Alignment Scores:
Pred. No.: 5.08e-09 Length: 97
Score: 157.50 Matches: 45
Percent Similarity: 32.67% Conservative: 21
Best Local Similarity: 22.28% Mismatches: 26
Query Match: 7.03% Indels: 110
DB: 11 Gaps: 1

US-09-788-074-2 (1-1279) x Q9QV90 (1-97)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 3 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 22
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 23 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 42
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACAGCAGCTGTATGCGGAGAAACACTGAGGTCAGC 310
Db 43 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 61
QY 311 TACAACATCTGTGGAAGCGACAGACGCTTCTAGATTTACAGATTAAATTTGCATTAACAAT 370
Db 61 ----- 61
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGCGAGTTGACTTTTGATA 430
Db 61 ----- 61
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 61 ----- 61
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QY 491 GCACATAGTTGTTATGTGAACAAATACAGTATGATGGGTGGAGTTCACAGAGGAAAGG 550
Db 61 ----- 61
QY 551 CGAAGACTTTGGAGTGGTGGTCCCTGGGGTTCCTTCACTTTTGGAGATGATGAAC 610
Db 61 ----- 61
QY 611 TAACTACCTGTTATTTTTCAGAGCGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 62 -----LeuValThrLeuAspGlyGlyLeuIleHisVa 73
QY 671 CCAGCAATGGACGGAAGAGACGACGATACAAAGAAACTGAAGGATGGGAAGATGAT 730
Db 73 LGInLysTrpAsnGlyClnGluThrThrLeuThrArgGluArgValAspGlyLysLeuI 93
QY 731 CGTG 734
Db 93 eLeu 94
RESULT 12
ID Q90WI9 PRELIMINARY; PRT; 53 AA.
AC Q90WI9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Fatty acid binding protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLAY; TISSUE=BLOOD;
RA Wang Q., Li N., Deng X.;
RT "Cloning and sequencing of fatty acid binding protein gene in
RT = chicken.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332700; AAK50883.1; -.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
FT NON_TER 1
FT NON_TER 53
SQ SEQUENCE 53 AA; 5681 MW; 3CAC59C5B6EC57FF CRC64;
Alignment Scores:
Pred. No.: 8.41e-09 Length: 53
Score: 155.00 Matches: 31
Percent Similarity: 77.36% Conservative: 10
Best Local Similarity: 58.49% Mismatches: 12
Query Match: 6.92% Indels: 0
DB: 13 Gaps: 0
US-09-788-074-2 (1-1279) x Q90WI9 (1-53)
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCAGCTGTATCATTACG 190
Db 1 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 20
QY 191 TGTGATGGCAACATCATCGGTCAAACCGAGACGACAGTGAAGACGACTGTGTCTCT 250
Db 21 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysSerThrGluIleSer 40
QY 251 TGTAACTGGGAGAGAGATTTGTATGAACACAGCAGCTGAT 289
Db 41 PheLysLeuGlyGluGluPheAspGluThrThrAlaAsp 53
RESULT 13
O57665 PRELIMINARY; PRT; 134 AA.
ED O57665
AC O57665;
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCAGCTGTATCATTACG 190
Db 1 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 20
QY 191 TGTGATGGCAACATCATCGGTCAAACCGAGACGACAGTGAAGACGACTGTGTCTCT 250
Db 21 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysSerThrGluIleSer 40
QY 251 TGTAACTGGGAGAGAGATTTGTATGAACACAGCAGCTGAT 289
Db 41 PheLysLeuGlyGluGluPheAspGluThrThrAlaAsp 53
RESULT 13
O57665 PRELIMINARY; PRT; 134 AA.
ED O57665
AC O57665;
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCAGCTGTATCATTACG 190
Db 1 GlyValGlyPheAlaThrArgGlnValGlyAsnArgThrLysProAsnLeuValIleSer 44
QY 191 TGTGATGGCAACAAC---ATCACGGTCAAACCGAGACGACAGTGAAGACGACTGTGTCTC 247
Db 45 ValAspAspGlnGlyPheValCysLeuLysSerGlnSerThrPheLysThrThrGluIle 64
QY 248 TCTTGTAACTGGGAGAGAGATTTGTATGAACACAGCAGCTGTATGAAGAAAAGTGGGTC 307
Db 65 LysPheLysLeuAsnGluProPheGluGluThrThrAlaAspAspArgLysThr-Arg-- 83
QY 308 AGCTACAACATACTGTGGAAGCGACAGAGAGCTTCTAGATTTACAGATTAATTCATTAC 367
Db 83 ----- 83
QY 368 AATGCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTCATTTTC 427
Db 83 ----- 83
QY 428 ATAAATTAGTAAAGTCCAGGACTAAGAATGAAGACATCTTATGAGTTCTTAGATCGA 487
Db 83 ----- 83
QY 488 AAAGCACATAGTTGTTATTGTTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAA 547
Db 83 ----- 83
QY 548 AGCGGAAGACTTGTGGAGTGGTGTGGGTCTCTGGGGTCTCTTACTTTTGAAGATGATG 607
Db 83 ----- 83
QY 608 AACTAACTACCCTGTATTTTTCGACAGCGGTCTGCACCTCCCAAGACGGTGCCTGTCTCA 667
Db 84 -----ThrValValThrLeuGluAsnGlyLysLeuValG 95
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DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Gobionotothen gibberifrons (Humped rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Gobionotothen.
OX NCB1_TaxID=36202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92446; AAC60354.1; -.
DR HSSP; P10790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15152 MW; D16BCFD514A2B268 CRC64;
Alignment Scores:
Pred. No.: 1.08e-08 Length: 134
Score: 155.00 Matches: 45
Percent Similarity: 31.07% Conservative: 19
Best Local Similarity: 21.84% Mismatches: 31
Query Match: 6.92% Indels: 11
DB: 13 Gaps: 2
US-09-788-074-2 (1-1279) x O57665 (1-134)
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCAGCTGTATCATTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnArgThrLysProAsnLeuValIleSer 44
QY 191 TGTGATGGCAACAAC---ATCACGGTCAAACCGAGACGACAGTGAAGACGACTGTGTCTC 247
Db 45 ValAspAspGlnGlyPheValCysLeuLysSerGlnSerThrPheLysThrThrGluIle 64
QY 248 TCTTGTAACTGGGAGAGAGATTTGTATGAACACAGCAGCTGTATGAAGAAAAGTGGGTC 307
Db 65 LysPheLysLeuAsnGluProPheGluGluThrThrAlaAspAspArgLysThr-Arg-- 83
QY 308 AGCTACAACATACTGTGGAAGCGACAGAGAGCTTCTAGATTTACAGATTAATTCATTAC 367
Db 83 ----- 83
QY 368 AATGCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTCATTTTC 427
Db 83 ----- 83
QY 428 ATAAATTAGTAAAGTCCAGGACTAAGAATGAAGACATCTTATGAGTTCTTAGATCGA 487
Db 83 ----- 83
QY 488 AAAGCACATAGTTGTTATTGTTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAA 547
Db 83 ----- 83
QY 548 AGCGGAAGACTTGTGGAGTGGTGTGGGTCTCTGGGGTCTCTTACTTTTGAAGATGATG 607
Db 83 ----- 83
QY 608 AACTAACTACCCTGTATTTTTCGACAGCGGTCTGCACCTCCCAAGACGGTGCCTGTCTCA 667
Db 84 -----ThrValValThrLeuGluAsnGlyLysLeuValG 95
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QY 668 GCACCAGCAATGGGACGGGAAGAGGAGCAGCAGATACACAGAAACTGAAGGATGGGAAGAT 727
      |   ||| ||||| ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 95 nlysGlnSerTrpAspGlyLysGluThrAsnIleGluArgGluIleGluAspGlyLysLe 115

QY 728 GATCGTGGTGACATC 743
      |   ||| |||
Db 115 uValAlaLysCysIle 120

RESULT 14
Q918N9
ID Q918N9 PRELIMINARY; PRT; 132 AA.
AC Q918N9:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Brain-type fatty-acid binding protein.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Denovan-Wright E.M., Pierce M., Wright J.M.;
RT "Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
RT binding protein and its tissue-specific expression in adult zebrafish
RT (Danio rerio).";
RL Biochim. Biophys. Acta 0:0-0(2000).
DR EMBL; AF237712; AAF79948.1; -.
DR HSSP; PI0790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin_1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;

Alignment Scores:
Pred. No.: 1, 23e-08 Length: 132
Score: 154.50 Matches: 46
Percent Similarity: 34.16% Conservative: 23
Best Local Similarity: 22.77% Mismatches: 23
Query Match: 6.90% Indels: 110
DB: 13 Gaps: 3

US-09-788-074-2 (1-1279) x Q918N9 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrIleValIleSer 44

QY 191 TGTGATGGCAACATCATCAGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTCT 250
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45 HisGluGlyAspLysValIleLysThrLeuSerThrPheLysAsnThrGluIleSer 64

QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACACGAGCTGATGGCAGAAAAACTGAGGTCACC 310
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 PheLysLeuGlyGluGluPheAspGluThrThrAlaAspArg-HisValLysSer-- 83

QY 311 TACAACATCTGTGAAGCCAGACAGACTCTTAGATTACAGATTAAATTCATTAACAAT 370
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 -----ThrVa 85

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 lSerLeu----- 87

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCCAAAA 490
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 ----- 87
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QY 491 GCACATAGTTGTATTGTGAACAATAATCAGTATGATGGGTGGAGTTTCAGAGGGAAGG 550
      |   ||| ||||| ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db 88 -----GluI 89

QY 551 CGAAGACTTGTGGAGTGGTGTGGTCTCTGGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
      |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 yAspAsn----- 91

QY 611 TAACTACCCCTGTATTTTTTCAGACGGTCTGCACCTTCCAAGACGGTCCCTGGTCCAGCA 670
      |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 -----LeuValGlnVa 95

QY 671 CCAGCAATGGGACGGGAAGGAGCAGCAGTACACAGAAAACTGAAGGATGGGAAGATGAT 730
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 lclnArgTrpAspGlyLysGluThrLysPheValArgGluIleLysAspGlyLysMetVa 115

QY 731 CGTG 734
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Db 115 lMet 116

RESULT 15
O57663
ID O57663 PRELIMINARY; PRT; 134 AA.
AC O57663:
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RT heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92444; AAC60352.1; -.
DR HSSP; PI0790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; Lipocalin_1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15182 MW; D4CBFCDF50E131968 CRC64;

Alignment Scores:
Pred. No.: 2, 4e-08 Length: 134
Score: 152.00 Matches: 45
Percent Similarity: 31.07% Conservative: 19
Best Local Similarity: 21.84% Mismatches: 31
Query Match: 6.79% Indels: 111
DB: 13 Gaps: 2

US-09-788-074-2 (1-1279) x O57663 (1-134)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnArgThrLysProAsnLeuValIleSer 44

QY 191 TGTGATGGCAACAAC---ATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTC 247
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45 ValAspAspGlnGlyPheValCysLeuLysSerGlnSerThrPheLysThrThrGluIle 64

QY 248 TCTTGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGGTC 307
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 LysPheLysLeuAsnGluProPheGluGluThrThrAlaAspArgLysThr-Arg-- 83
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```
QY 308 AGCTACACATACTGTGAAGCGACAGACAGCTTCTAGATTTACAGATTAATTTGCATTAAC 367
Db 83 ----- 83
QY 368 AATGCTGTACTTACTGCGCAAGGGCTGACTGAAAAACTACTTTATGGAGTTGACTTTTG 427
Db 83 ----- 83
QY 428 ATAAATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATCAGTTTCTAGATCGA 487
Db 83 ----- 83
QY 488 AAAGCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAA 547
Db 83 ----- 83
QY 548 AGCGGAAGACTTGTGGAGTGGTGGGTCTCTGGGGTTCCTTCACTTTGGGAAGATGATG 607
Db 83 ----- 83
QY 608 AACTRACTACCCCTGTATTTTTCGACAGCGGTCTGCACCTTCCAAGACGGTGCCCTGGTCCA 667
Db 84 -----ThrValValThrLeuGluAsnGlyLysLeuValG1 95
QY 668 GCACCAGCAATGGCGGAGGAGGACGACGATACACAGAAAACCTCAAGGATGGGAAGAT 727
Db 95 nLysGlnCysTrpaspGlyLysGluThrAsnIleGluArgGluIleGluaspGlyLysLe 115
QY 728 GATCGTGGTGAGCATC 743
Db 115 uValAlaLysCysIle 120
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Search completed: November 25, 2002, 10:30:58
Job time : 90.5 secs

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:12 ; Search time 21 Seconds
(without alignments)
5052.212 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 2239
Sequence: 1 aatggagcaacatgctagc.....tctatgagaaggtgcaatga 1279

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cpn2.1/USPTO.spool/US09788074/runat_25112002_093513_15663/app_query.fasta_1.1415
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=human40.coi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09788074.ecgn_1.1.27.@runat_25112002_093513_15663 -NCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406.5	18.2	135	1 FABLE_MOUSE	Q05816 mus musculus
2	367.5	16.4	135	1 FABLE_RAT	P55053 rattus norv
3	350.5	15.7	135	1 FABLE_HUMAN	Q01469 homo sapien
4	334.5	14.9	135	1 FABLE_BOVIN	P55052 bos taurus
5	200.5	9.0	131	1 MYP2_RABIT	P02691 oryctolagus
6	189.5	8.5	131	1 MYP2_HUMAN	P02689 homo sapien
7	187.5	8.4	131	1 FABA_PIG	Q91788 sus scrofa
8	182.5	8.2	131	1 FABA_SPECTR	Q99p60 spermophilu
9	181.5	8.1	132	1 FABL_GINCI	P80049 ginglymosto
10	180.5	8.1	132	1 FABA_BOVIN	P48035 bos taurus
11	177.5	7.9	131	1 MYP2_MOUSE	P24526 mus musculus
12	176.5	7.9	132	1 FABL_RAT	P07483 rattus norv
13	175.5	7.8	131	1 MYP2_BOVIN	P02690 bos taurus
14	174.5	7.8	131	1 FABA_HUMAN	P15090 homo sapien
15	174	7.8	131	1 FABA_MOUSE	P04117 mus musculus
16	171.5	7.7	132	1 FABL_HUMAN	P05413 homo sapien
17	171.5	7.7	132	1 FABL_SPECTR	Q99p51 spermophilu
18	169.5	7.6	132	1 FABL_PIG	O02772 sus scrofa

19	163.5	7.3	132	1 FABL_MOUSE	P11404 mus musculus
20	159	7.1	114	1 FABL_LAMJA	P82188 lampetra ja
21	158.5	7.1	132	1 FABL_BOVIN	P10790 bos taurus
22	155.5	6.9	131	1 FABB_CHICK	Q05423 gallus gall
23	152	6.8	131	1 FABA_RAT	P70623 rattus norv
24	151.5	6.8	131	1 FABB_HUMAN	O15540 homo sapien
25	150.5	6.7	132	1 FABB_BOVIN	Q09139 bos taurus
26	148	6.6	132	1 FABL_ONCMY	O13008 oncorhynchu
27	139.5	6.2	131	1 FABB_MOUSE	P51880 mus musculus
28	136.5	6.1	131	1 FABB_RAT	P55051 rattus norv
29	132.5	5.9	132	1 TLBP_MOUSE	O08716 mus musculus
30	132.5	5.9	132	1 TLBP_RAT	P55054 rattus norv
31	128.5	5.7	120	1 RET3_CHICK	P40220 gallus gall
32	122	5.4	136	1 RET3_FUGRU	O42386 fugu rubrip
33	121	5.4	137	1 RET3_XENLA	P50568 xenopus lae
34	120	5.4	136	1 RET3_HUMAN	P29762 homo sapien
35	119	5.3	136	1 RET3_MOUSE	P02695 mus musculus
36	118	5.3	137	1 RET4_HUMAN	P29373 homo sapien
37	117	5.2	133	1 FAPP_ECHGR	Q002970 echinococcu
38	109	4.9	133	1 FAPP_SCHMA	P29498 schistosoma
39	108	4.8	137	1 RET4_MOUSE	P22935 mus musculus
40	103	4.6	134	1 RET5_HUMAN	P82980 homo sapien
41	102	4.6	134	1 RET1_HUMAN	P09455 homo sapien
42	102	4.6	134	1 RET1_MOUSE	Q00315 mus musculus
43	102	4.6	134	1 RET1_RAT	P02596 rattus norv
44	101.5	4.5	134	1 RET7_HUMAN	Q96705 homo sapien
45	99	4.4	131	1 FAPP_LEPOS	Q9u5p1 lepidoglyph

ALIGNMENTS

RESULT 1	FABLE_MOUSE	STANDARD;	PRT;	135 AA.
AC	Q05816;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (Keratinocyte lipid-binding protein).			
DE	FABP5 OR MALI OR KLBP OR FABPE.			
GN	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Keratinocytes;			
RX	MEDLINE=93352523; PubMed=8349619;			
RA	Krieg P., Feil S., Fuerstenberger G., Bowden T.G.;			
RT	"Tumor-specific overexpression of a novel keratinocyte lipid-binding protein. Identification and characterization of a cloned sequence activated during multistage carcinogenesis in mouse skin.";			
RL	J. Biol. Chem. 268:17362-17369(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RX	MEDLINE=98332726; PubMed=9666100;			
RA	Bleck B., Hohoff C., Binns B., Rustow B., Dixkens C., Hameister H., Boerchers T., Spener F.;			
RT	"Cloning and chromosomal localisation of the murine epidermal-type fatty acid binding protein gene (fabpe).";			
RL	Gene 215:123-130(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=99013878; PubMed=9795232;			
RA	Hertzel A.V., Bernlohr D.A.;			
RT	"Cloning and chromosomal location of the murine Keratinocyte lipid-binding protein gene.";			
RL	Gene 221:235-243(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			

RC STRAIN=C57BL/6J; TISSUE=Stomach;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bulc T., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC C18 CHAIN LENGTH (BY SIMILARITY).
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.
 CC !- TISSUE SPECIFICITY: MOST ABUNDANT IN KERATINOCYTES AND ALSO IN
 CC STRATIFIED EPITHELIA OF EPIDERMIS AND TONGUE. RELATIVELY HIGH
 CC LEVELS FOUND IN ADIPOSE AND MAMMARY TISSUES AND SMALL AMOUNTS
 CC FOUND IN HEART, BRAIN, LIVER, SPLEEN, MUSCLE AND LUNG.
 CC !- SIMILARITY: BELONGS TO THE FABP/P2/CBPP/CRAFP FAMILY OF
 CC TRANSPORTERS.
 CC
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 CC
 CC EMBL; X70100; CAA49703.1; -;
 DR EMBL; AJ223066; CAA11069.1; -;
 DR EMBL; AF061015; AAC82368.1; -;
 DR EMBL; AF061014; AAC82368.1; JOINED.
 DR EMBL; AK008782; BAB25890.1; -;
 DR EMBL; AK011551; BAB27692.1; -;
 DR EMBL; BC002008; AAH02008.1; -;
 DR PIR; S36635; S36635.
 DR HSSP; Q01469; 1B56.
 DR MGD; MGI:101790; Fapp5.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipoclin_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding.
 SQ SEQUENCE 135 AA; 15137 MW; 6A6C8DBEBB046185 CRC64;
 Alignment Scores:
 Pred. No.: 2 62e-32 Length: 135
 Score: 406.50 Matches: 93
 Percent Similarity: 45.02% Conservative: 2
 Best Local Similarity: 44.08% Mismatches: 6
 Query Match: 18.16% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x FABE_MOUSE (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGCAGCTGTATCATTCAG 190
 DB |||||
 QY 27 GlyValGlyLeuAlaLeuArgLysMetAlaAlaMetAlaLysProAspCysIleIleThr 46
 DB |||||
 QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGCAGCAGTGAAGCAGCTGTGTCTCT 250
 DB |||||
 QY 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrThrValPheSer 66
 DB |||||
 QY 251 TGTAACTCTGGGAGAGAAGTTTGTATGAACGACACAGCTGTGGCGCAAAACCTGAGGTGACG 310
 DB |||||
 QY 67 CysAsnLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
 DB |||||
 QY 311 TACAACATACTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATTCATTAACAAT 370
 DB |||||
 QY 85 ----- 85
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAACAACTACTTTATGGAGTTGACTTTTGATA 430
 DB |||||
 QY 85 ----- 85
 QY 431 AATTAGTAAAGTCCCGAGCGTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 DB |||||
 QY 85 ----- 85
 QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
 DB |||||
 QY 85 ----- 85
 QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGGGTTCCTTCTACTTTTGGAGAGTGAAC 610
 DB |||||
 QY 611 TAACTACCCCTGTATTTTTCAGACGGTGTGCACCTTCCCAAGCGGTGCCCTGGTCCAGCA 670
 DB |||||
 QY 86 -----valCysThrPheGlnAspGlyAlaLeuValGlnHI 97
 DB |||||
 QY 671 CCAGCAATGGGCGGAGGAGGACGACGATACAAAGAACTGAAGATGGGAGATGAT 730
 DB |||||
 QY 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetII 117
 QY 731 CGTGGTGACATCAAGCACTGGCACCATGC 761
 DB |||||
 QY 117 eValGluCysValMetAsnAlaThrCys 127
 DB |||||
 RESULT 2
 FABE_RAT
 ID FABE_RAT STANDARD; PRT; 135 AA.
 AC P55053; P97757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Fatty acid-binding protein, epidermal (E-FABP) (Cutaneous fatty acid-
 DE binding protein) (C-FABP) (DALI).
 GN FABP5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lens;
 RX MEDLINE=95331629; PubMed=7607553;
 RA Wen Y., Li G.W., Chen P., Wong E., Bekhor I.;
 RT "Lens epithelial cell mRNA. II. Expression of a mRNA encoding a
 RT lipid-binding protein in rat lens epithelial cells.";
 RL Gene 158:269-274(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Skin;
 RX MEDLINE=94220094; PubMed=8166694;
 RA Watanabe R., Fujii H., Odani S., Sakakibara J., Yamamoto A., Ito M.,
 RA Ono T.;
 RT "Molecular cloning of a cDNA encoding a novel fatty acid-binding

RT protein from rat skin.";
 RL Biochem. Biophys. Res. Commun. 200:253-259(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Nerve;
 RX MEDLINE=96302634; PubMed=8723767;
 RA de Leon M., Welcher A.A., Nahin R.H., Liu Y., Ruda M.A.,
 RA Shooter E.M., Molina C.A.;
 RT "Fatty acid binding protein is induced in neurons of the dorsal root
 RT ganglia after peripheral nerve injury.";
 RL J. Neurosci. Res. 44:283-292(1996).
 RL -|- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC C18 CHAIN LENGTH (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.
 CC -----
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 CC -----
 CC EMBL; U13253; AAA66680.1; -;
 DR EMBL; S69874; AAB30574.1; -;
 DR EMBL; S83247; AAB46848.1; -;
 DR HSSP; O01469; 1B56.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding.
 FT CONFLICT 49 49 G -> N (IN REF. 1).
 FT CONFLICT 112 112 K -> N (IN REF. 3).
 FT SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 135
 Score: 367.50 Length: 135
 Percent Similarity: 43.13% Matches: 85
 Best Local Similarity: 40.28% Conservative: 6
 Query Match: 16.41% Mismatches: 10
 Indels: 110
 Gaps: 1
 DB: 1
 US-09-788-074-2 (1-1279) x FABE_RAT (1-135)
 QY 131 GGAGTAGGACTGGCTTATAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
 Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACACATCATCGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 47 LeuAspGlyAsnAsnThrValLysThrGluSerThrValLysThrValPheSer 66
 QY 251 TGTAACTCGGAGAGAGTGTGATGAACACGACAGCTGATGGCAGAAAACACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGluLysPheAspGluThrAlaAspGlyArgLysThrGlu-Thr--- 85
 QY 311 TACAACATCTCTGTGAAGCGACGACAGACTTCTAGATTACAGATTAATGTCATTAACAAT 370
 Db 85 ----- 85
 QY 371 GTCGTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 85 ----- 85
 QY 431 AATTAGTAAAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 85 ----- 85

QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 85 ----- 85
 QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 85 ----- 85
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTCCCTGTGCCAGCA 670
 Db 86 -----ValCysThrPheThrAspGlyAlaLeuValGlnH1 97
 QY 671 CCAGCAATGGGACGGGAGGAGGACGACGATACAAAGAAACTGAAGATGGGAGATGAT 730
 Db 97 sGlnLysTrpGluGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetVa 117
 QY 731 CGTGGTGAGACTCAAAAGCAGCTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnAlaIleCys 127
 RESULT 3
 FABE_HUMAN
 ID FABE_HUMAN STANDARD; PRT; 135 AA.
 AC Q01469;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
 DE fatty acid-binding protein homolog) (PA-FABP).
 GN FABP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=92381332; PubMed=1512466;
 RA Madsen P.S., Rasmussen H.H., Leffers H., Honore B., Cells J.E.;
 RT "Molecular cloning and expression of a novel keratinocyte protein
 RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
 RT highly up-regulated in psoriatic skin and that shares similarity to
 RT fatty acid-binding proteins.";
 RL J. Invest. Dermatol. 99:299-305(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
 RX TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [4]
 RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
 RX MEDLINE=94379963; PubMed=8092987;
 RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
 RA Hellman U., Saurat J.-H.;
 RT "Purification and characterization of the human epidermal fatty acid-
 RT binding protein: localization during epidermal cell differentiation
 RT in vivo and in vitro.";
 RL Biochem. J. 302:363-371(1994).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RX MEDLINE=99425110; PubMed=10493790;
 RA Hohoff C., Borchers T., Rustow B., Spener F., van Tilbeurgh H.;
 RT "Expression, purification and crystal structure determination of
 RT recombinant human epidermal-type fatty acid-binding protein.";

RL Biochemistry 38:12229-12239(1999).
 CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING
 CC DOUBLE BONDS REDUCES THE AFFINITY. MAY BE INVOLVED IN KERATINOCYTE
 CC DIFFERENTIATION.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
 CC SKIN.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; M94856; AAA58467.1; -.
 DR EMBL; BC019385; AAH19385.1; -.
 DR PDB; 1B56; 05-OCT-99.
 DR Aarhus/Ghent-2DPAGE; 3007; IEF.
 DR Genew; HGNC:3560; FABP5.
 DR MIM; 605168; -.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding; 3D-structure.
 SQ SEQUENCE 135 AA; 15164 MW; 77D38F8806143D63 CRC64;

Alignment Scores:
 Pred. No.: 9,66e-27 Length: 135
 Score: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FABE_HUMAN (1-135)

QY 131 GGAGTAGGACTGCTCTTAGGAGATGGCTGCCATGCCAAGCAGACTGTATCATTCAG 190
 Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCATCGGTCACAAACCGAGAGACAGTGAAGCAGTGTGTTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGCATGGCAAGAAACACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGlyLysPheGluGluThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACTGTGAACCGCAGAGAAGCTTCTAGATTACAGATTAAATTGCAATTAACAAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAGGGCTGACTGAAACAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 ----- 84
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGCAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGATTGTGAACAAATACGATGATGGGTGGAGTTCAGAGAGGGAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 610

..

Db 84 ----- 84
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCCTGGTCCACCA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnH1 97
 QY 671 CCAGCAATGGGACGGGAGGAGAGCAGCAGTAAACAGAAACTGAAGATGGGAAGATCAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVal 117
 QY 731 CGTGGTGCAGTCATCAACACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 4
 FABE_BOVIN STANDARD; PRT; 135 AA.
 AC P55052; O62808;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Fatty acid-binding protein, epidermal (E-FABP) (Differentiation-
 DE associated lipid binding protein LP2).
 GN FABP5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129.
 RC TISSUE=Lens;
 RX MEDLINE=97103094; PubMed=8947466;
 RA Jaworski C, Wistow G.;
 RT "LP2, a differentiation-associated lipid-binding protein expressed in
 RT bovine lens.";
 RL Biochem. J. 320:49-54(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Retina;
 RX MEDLINE=98198033; PubMed=9521644;
 RA Kingma P.B., Bok D., Ong D.E.;
 RT "Bovine epidermal fatty acid-binding protein: determination of ligand
 RT specificity and cellular localization in retina and testis.";
 RL Biochemistry 37:3250-3257(1998).
 CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN
 CC THE UPTAKE AND TRANSPORT OF FATTY ACIDS ESSENTIAL FOR THE
 CC NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL
 CC TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND RETINA (FOUND IN THE
 CC MUELLER CELLS), MODERATELY ABUNDANT IN HEART AND TESTIS (FOUND IN
 CC THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; U55188; AAB41297.1; -.
 DR EMBL; AF059507; AAC14711.1; -.
 DR HSSP; Q01469; 1B56.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.

Db 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSer-- 82
 QY 311 TACAACATACCTGTGACGACGACAGAGCTTCTAGATTACAGATTAAATGCATTAAACAAT 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTACTCCCAAGGCTGACTGAAAACTACTTTATGGAGTTGACTTTTCATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTTATGTGAACAAATACATGATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
 Db 82 ----- 82
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 610
 Db 82 ----- 82
 QY 611 TAACACTACCTGTATTTTTCAGACGGTGTGACCTTCCAAAGACGGTCCCTGCTCCAGCA 670
 Db 83 ----- 111
 QY 671 CCAGCAATGGACGGAAGGAGCAGCAGTAAACAAGAACTCAAGGATGGGAGATGAT 730
 Db 94 lGlnLysTrpAspGlyLysGluThrThrLysArgLysLeuValAspGlyLysMetVa 114
 QY 731 CGTG 734
 Db 114 lval 115
 RESULT 6
 MYP2_HUMAN STANDARD; PRT; 131 AA.
 AC P02689;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P2 protein.
 GN PMP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92068191; PubMed=1720307;
 RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
 RA Uyemura K.;
 RT "Isolation and sequence determination of cDNA encoding P2 protein of
 RT human peripheral myelin.";
 RL Biochem. Biophys. Res. Commun. 181:204-207(1991).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=83058785; PubMed=6183401;
 RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
 RT "The complete amino acid sequence of human P2 protein.";
 RL J. Neurochem. 39:1759-1762(1982).
 RN [3]
 RP SEQUENCE OF 1-115 FROM N.A.
 RX MEDLINE=95054012; PubMed=7525873;
 RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
 RA Tennekoon G.;
 RT "Partial structure and mapping of the human myelin P2 protein gene.";
 RL J. Neurochem. 63:2010-2013(1994).
 CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
 CC CELLS.
 CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
 CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
 CC PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.

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CC EMBL: D16181; BAA03726.1;
 DR EMBL: D16179; BAA03726.1; JOINED.
 DR EMBL: D16180; BAA03726.1; JOINED.
 DR EMBL: X62167; CAA44096.1;
 DR EMBL: S73470; AAB32592.2;
 DR EMBL: S73468; AAB32592.2; JOINED.
 DR EMBL: S73469; AAB32592.2; JOINED.
 DR PIR: A03143; MPH02.
 DR PIR: JT0977; JT0977.
 DR HSP: P02690; 1PMP.
 DR Genew: HGNC:9117; PMP2.
 DR MIM: 170715;
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR Pfam: PF00061; lipocalin; 1.
 DR PRINTS: PR00178; FATTYACIDBP.
 DR PROSITE: PS00214; FABP; 1.
 KW Myelin; Lipid-binding; Transport; Acetylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT DISULFID 117 124 G -> GG (IN REF. 3).
 FT CONFLICT 24 24 D -> N (IN REF. 2).
 FT CONFLICT 98 98 N -> D (IN REF. 2).
 FT CONFLICT 110 110
 SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Alignment Scores:

Pred. No.: 9.76e-11 Length: 131
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservative: 16
 Best Local Similarity: 26.37% Mismatches: 22
 Query Match: 8.46% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_HUMAN (1-131)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATACG 190
 Db 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleSer 43
 QY 191 TGTGATGGCAACACATCACGGTCAAAACCGAGAGCACAGTGAAGAGCTGTGTCTCT 250
 Db 44 LysLysGlyAspIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 63
 QY 251 TGTAACTGGGAGAGAAGTTGTATGAACACACAGCTGATGGCAAGAAACTGAGGTCA 310
 Db 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSer-- 82
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATGCATTAAACA 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAACTACTTTATGGAGTTGACTTTTCATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTTATGTGAACAAATACATGATGATGGGTGGAGTTTCAGAGAGGAAAG 550


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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spermophilus.
OC NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittel D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding
RT proteins in hibernating ground squirrels."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF327855; AAK08084.1; .
DR HSP; P04117; ILID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14634 MW; FCEE7B092A2AF708 CRC64;
Alignment Scores:
Pred. No.: 4.85e-10 Length: 131
Score: 182.50 Matches: 50
Percent Similarity: 33.66% Conservative: 18
Best Local Similarity: 24.75% Mismatches: 24
Query Match: 8.15% Indels: 110
DB: Gaps: 1
US-09-788-074-2 (1-1279) x FABA_SPETR (1-131)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGCCTGCCATGCCAAGCCAGACTGTATCATTAAG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 43
QY 191 TGTGATGGCAACACATCATCGGTCAAAACCCAGAGACACTGAAGACGACTGTGTTCTCT 250
Db 44 ValAsnGlyAspValIleThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTCGGAGAGAAGTTTGATGAACACACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValIysSer-- 82
QY 311 TACAACATACTGTGAACGCGACAGAAGCTCTTAGATTACAGATTAATAATTCATTAACAAT 370
Db 82 ----- 82
QY 371 GTCTGACTTACTGCCNAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAAAGTCCCGAGGACTAAGAAATCAAGACATCTTTATGAGTTTCTAGATCGAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGCGGAAGG 550

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Db	82	-----	82
QY	551	CGAAGACTTGTGGAGTGGTGGGTCTGGGGTCTTCACTTTGGGAAGATGATGAAC	610
Db	82	-----	82
QY	611	TAACTACCCGTATTTTTCGACAGCGTCTCCACTTCCAAAGACGGTGCCTGGTCCAGCA	670
Db	83	-----	83
QY	671	CCAGCAATGGGACGGGAGGAGCAGCATAACAAAGAACTCAAGGATGGGGAAGATGAT	730
Db	94	lGlnlYstrpAspGlyLysSerThrIrlleLysArgLysArgLysAspLysLeuVa	114
QY	731	CGTG 734	
Db	114	lVal 115	
RESULT 9			
FABL_GINCI			
ID	FABL_GINCI	STANDARD;	PRT; 132 AA.
AC	P80049;		
DT	01-MAR-1992 (Rel. 21, Created)		
DT	01-MAR-1992 (Rel. 21, Last sequence update)		
DT	01-JUN-1994 (Rel. 29, Last annotation update)		
DE	Fatty acid-binding protein, liver (L-FABP).		
OS	Ginglymostoma cirratum (Nurse shark)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;		
OC	Ginglymostomatidae; Ginglymostoma.		
OX	NCBI_TaxID=7801;		
RP	[1]		
RP	SEQUENCE.		
RC	TISSUE=Liver;		
RA	MEDLINE=92137215; PubMed=1735421;		
RX	Medzhiradzsky K.F., Gibson B.W., Kaur S., Yu Z., Medzhiradzsky D.,		
RA	Burlingame A.L., Bass N.M.;		
RT	"The primary structure of fatty-acid-binding protein from nurse shark		
RT	liver. Structural and evolutionary relationship to the mammalian		
RT	fatty-acid-binding protein family";		
RL	Eur. J. Biochem. 303:327-339(1992).		
CC	-1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR		
CC	TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.		
CC	-1- SUBCELLULAR LOCATION: CYTOSOLM1C.		
CC	-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF		
CC	TRANSPORTERS.		
DR	PIR; S20297; S20297.		
DR	HSSP; P05413; 1HMT.		
DR	InterPro; IPR000463; Fatty acid BP.		
DR	InterPro; IPR000586; Lipocin_cytFABP.		
DR	Pfam; PF00061; Lipocalin; 1.		
DR	PRINTS; PR00178; FATTYACIDBP.		
DR	PROSITE; PS00214; FABP; 1.		
KW	Transport; Lipid-binding; Acetylation; Phosphorylation.		
FT	MOD_RES 1 1		
FT	MOD_RES 19 19		
FT	ACETYLATION.		
FT	PHOSPHORYLATION (BY TYR-KINASES).		
FT	(POTENTIAL).		
SEQ	SEQUENCE 132 AA; 15079 MW; 2AFDEA2C0BE2095F CRC64;		
Alignment Scores:			
Pred. No.:	6.1e-10	Length:	132
Score:	181.50	Matches:	53
Percent Similarity:	34.33%	Conservative:	16
Best Local Similarity:	26.37%	Mismatches:	22
Query Match:	8.11%	Indels:	110
DB:	1	Gaps:	2
US-09-788-074-2 (1-1279) x FABL_GINCI(1-132)			

Qy	134	GTAGGACTGGCTCTTAGGAGATGGTGGCATGGCCAGCCAGACTGTATCATTTACGTGT	193
		:	
Db	25	ValSerLeuAlaGlnArgLysValAlaThrThrValLysProLysThrIleIleSerLeu	44


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QY 194 GATGGCAACATCATCGCTCAAAACCGAGACAGACAGTGAAGACGACTGTGTTCTTCTTGT 253
Db 45 ASpglyAspVallelThrLysThrGluSerThrPheLysSerThrAsnIleGlnPhe 64
QY 254 AACCTGGGAGAGAAGTTTCATCAACAGCAGCTGATGGCAGAAACAACTCAGCTCAGCTAC 313
Db 65 LysLeuAlaGluPheAspGluThrThrAlaAspAsnArg----- 78
QY 314 AACATACCTGTAAGCGACAGAACTCTAGATTTACAGATTAAATGTCATTAAACATGTC 373
Db 78 ----- 78
QY 374 TGTACTACTGCCAAGGGCTGACTGAACAACTACTTTATGAGTTGACTTTTGATAAAT 433
Db 79 -----ThrThrLysThrThr----- 83
QY 434 TAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAGCA 493
Db 83 ----- 83
QY 494 CATAGTTGATTGTGAACAAATCATGATGATGGGGTGAGTTCAGAGAGGAAAGCGA 553
Db 83 ----- 83
QY -554 AGACTTGTGGAGTGTGGTCTGGGGTCTCTTCACTTTGGNAGATGATGAACATAA 613
Db 83 ----- 83
QY 614 CTACCTGTATTTTTCAGACAGCTGTGACCTTCAAGAGCTGCCCTGGTCCAGCACCA 673
Db 84 -----ValLysLeu-GluAsnGlyLysLeuValGlnThrG1 95
QY 674 GCAATGGGAGGAGGAGGAGCAGCAGTCAACAACTGAAGAGTGGGAAGATGATCGT 733
Db 95 nArgTpAspGlyLysGluThrThrLeuValArgGluLeuGlnAspGlyLysLeuIleLe 115
QY 734 G 734
Db 115 : 115
RESULT 10
FABA_BOVIN
ID FABA_BOVIN STANDARD; PRT; 131 AA.
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
GN FAPB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartezko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers F., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FAPB/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
DR EMBL; X89244; CAA61532.1; -
DR HSSP; P04117; LLID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;
Alignment Scores:
Pred. No.: 7,66e-10 Length: 131
Score: 180.50 Matches: 50
Percent Similarity: 32.18% Conservative: 15
Best Local Similarity: 24.75% Mismatches: 27
Query Match: 8.06% Indels: 110
DB: 1 Gaps: 1
US-09-788-074-2 (1-1279) x FABA_BOVIN (1-131)
QY 131 GGAGTAGGACTGCCTCTTAGGAAGATGGTCCATGCCAAGCCAGACACTGTATCATTCAG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProThrLeuIleIleSer 43
QY 191 TGTGTGGCAACAACATCATCGCTCAAAACCGAGACAGTGAAGACGACTGTGTTCTCT 250
Db 44 LeuAsnGlyGlyValThrThrLysSerGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTCGGAGAGAAGTTTGTATGAACAGCAGCTGTATGGCAGAAAACTGAGGTCA 310
Db 64 PheLysLeuGlyGlnGluPheAspGluIleThrProAspArg-LysValLysSer-- 82
QY 311 TACAACATACTGTGAAGCGACAGCAAGCTCTAGATTACAGATTAATTCATTAACAAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAAAATCAGTATCATGATGGGTGGAGTTTCAGAGAGG 550
Db 82 ----- 82
QY 551 CGAAGACTGTTGGAGTGGTGGTGGTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTTCAGACAGCTGTGCACCTTCCAAAGAGCGTCCCTGGTCCAGCA 670
Db 83 -----IleValAsnLeuAspGluGlyAlaLeuValGlnVa 94
QY 671 CCAGCAATGGGAGGAGGAGGAGCAGCAGTAAACAACTCAAGAGTGGGAAGATGAT 730
Db 94 lGlnAsnTrpAspGlyLysSerThrThrIleLysArgLysLeuMetAspLysMetVa 114
QY 731 CGTG 734
Db 114 lIleu 115
RESULT 11
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MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
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CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSP; P02690; LPMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR - InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Myelin; Lipid-binding; Transport; Acetylation.
KW MYELIN MET 0 BY SIMILARITY.
FT - INIT MET 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 1 1
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Alignment Scores:
Pred. No.: 1.52e-09 Length: 131
Score: 177.50 Matches: 52
Percent Similarity: 32.23% Conservative: 16
Best Local Similarity: 24.64% Mismatches: 33
Query Match: 7.93% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_MOUSE (1-131)
QY 131 GGAGTAGGACTGCTTTAGGAGATGGCTGCCATGGCCAGCCAGACTGTATCATAGC 190
Db 24 GlyValGlyLeuAlaAsnArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 43
QY 191 TGTGATGGCAACAACATACGCTGCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 44 LysLysGlyAspTyrIleThrIleArgThrGluSerAlaPheLysAsnThrGluIleSer 63
QY 251 TGTAACTGGGAGAGTTTGTGAACACACAGCTGGTGGCAGAAAAACTGAGGTTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheAspGluThrThrAlaAspAsnArgLysAla-LysSer-- 82
QY 311 TACAACATACTGTGAAGCCAGACAGACTTCTAGATTACAGATTAAATTGCATTACAAAT 370
Db 82 -----
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QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 82 -----
QY 431 AATTAGTAAAGTCCAGGAGCTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 82 -----
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 82 -----
QY 551 CGAAGACTTGTGGAGCTGCTGGGGTCTCTTCACTTTTGAAGATGATGAAC 610
Db 82 -----
QY 611 TAACTACCTGTATTTTGCAGCGTCTGCACCTTCCAGAGCGGTGCCCTGTGTCAGCA 670
Db 83 -----
QY 671 CCAGCAATGGGAGGAGGAGGAGCAGCATACACAAAACCTGACGATGGGGAAGATGAT 730
Db 94 LGLnLysTrpAspGlyLysGluThrAlaIleArgArgThrLeuLeuAspGlyArgMetVa 114
QY 731 CGTGGTGACATCAAGCACTGGCACCATGC 761
Db 114 IValGluCysIleMetLysGlyValValCys 124
RESULT 12
FABH_RAT
ID FABH_RAT STANDARD; PRT; 132 AA.
AC P07483; Q9QY04;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, heart (H-FABP).
OS FABP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=87250640; PubMed=3036869;
RA Heukeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
RT "Analysis of the tissue-specific expression, developmental regulation, and linkage relationships of a rodent gene encoding heart fatty acid binding protein.";
RL J. Biol. Chem. 262:9709-9717(1987).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=88107756; PubMed=3427112;
RA Clafey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
RT "Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: identical forms in heart and skeletal muscle.";
RL Biochemistry 26:7900-7904(1987).
RN [3]
SEQUENCE.
RP MEDLINE=88153733; PubMed=3162235;
RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
RT "Revision of the blocked N terminus of rat heart fatty acid-binding protein by liquid secondary ion mass spectrometry.";
RL J. Biol. Chem. 263:4182-4185(1988).
RN [4]
PRELIMINARY SEQUENCE.
RP MEDLINE=86250713; PubMed=2424895;
RA Sacchetti J.C., Said B., Schulz H., Gordon J.I.;
RT "Rat heart fatty acid-binding protein is highly homologous to the murine adipocyte 422 protein and the P2 protein of peripheral nerve myelin.";
RL J. Biol. Chem. 261:8218-8223(1986).
RN [5]
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RC SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=91170283; PubMed=2005132;
 RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;
 RT "Primary structure and cellular distribution of two fatty
 RT acid-binding proteins in adult rat kidneys.";
 RL J. Biol. Chem. 266:5963-5972(1991).
 RN [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Wistar; TISSUE=Heart;
 RC PubMed=10561574;
 RX Zhang J., Rickers-Haunerland J., Dawe I., Haunerland N.H.;
 RA "Structure and chromosomal location of the rat gene encoding the heart
 RT fatty acid-binding protein.";
 RT Eur. J. Biochem. 266:347-351(1999).
 RN [7]
 RN SEQUENCE OF 58-86.
 RX MEDLINE=89374061; PubMed=2775193;
 RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
 RT "Rat heart fatty acid-binding protein. Evidence that supports the
 RT amino acid sequence predicted from the cDNA.";
 RL Biochem. J. 260:303-306(1989).
 RN [8]
 RN PARTIAL SEQUENCE.
 RP TISSUE=Stomach;
 RC MEDLINE=90032682; PubMed=2806260;
 RX Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
 RA Matsubara Y., Muto T., Ono T.;
 RT "Purification and characterization of a fatty-acid-binding protein
 RT from the gastric mucosa of rats. Possible identity with heart
 RT fatty-acid-binding protein and its parietal cell localization.";
 RL Eur. J. Biochem. 185:27-33(1989).
 RN [9]
 RN PARTIAL SEQUENCE.
 RP TISSUE=Mammary gland;
 RC MEDLINE=88326235; PubMed=3415652;
 RX Jones P.D., Carne A., Bass N.M., Grigor M.R.;
 RA "Isolation and characterization of fatty acid binding proteins from
 RT mammary tissue of lactating rats.";
 RL Biochem. J. 251:919-925(1988).
 RN [10]
 RN PARTIAL SEQUENCE.
 RP TISSUE=Mammary gland;
 RC MEDLINE=94162301; PubMed=8117746;
 RX Nielsen S.O., Rump R., Hoerup P., Roepstorff P., Spener F.;
 RA "Differentiation regulation and phosphorylation of the fatty acid-
 RT binding protein from rat mammary epithelial cells.";
 RL Biochim. Biophys. Acta 1211:189-197(1994).
 CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
 CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
 CC BRAIN AND MAMMARY GLAND.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CBAP FAMILY OF
 CC TRANSPORTERS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02773; AAA41136.1; -;
 DR EMBL: M18034; AAA41137.1; -;
 DR EMBL: AF144090; AAF19003.1; -;
 DR PIR: A23838; A23838.
 DR PIR: A27452; A27452.
 DR PIR: A28197; A28197.
 DR PIR: A28458; A28458.
 DR PIR: A39551; A39551.
 DR PIR: S06478; S06478.

DR HSP: P05413; LHMT.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocalin_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
 FT CONFLICT 63 63 S -> SN (IN REF. 3).
 FT CONFLICT 69 69 E -> Q (IN REF. 5).
 FT CONFLICT 70 70 F -> D (IN REF. 3).
 FT CONFLICT 115 115 L -> LL (IN REF. 6).
 SQ SEQUENCE 132 AA; 14643 MW; 31B4C66A8BFB45BE CRC64;
 Alignment Scores:
 Pred. No.: 1.92e-09 Length: 132
 Score: 176.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
 Best Local Similarity: 24.75% Mismatches: 26
 Query Match: 7.88% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x FABH_RAT (1-132)
 QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGCTGTATCATACG 190
 Db 24 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 43
 QY 191 TGTGATGGCAACACATCAGCGGTCAAAACCGAGACAGTGAAGACGACTGTGTTCTCT 250
 Db 44 LysAsnGlyAspThrIleThrIleYThrHisSerThrPhelYsAsnThrGluIleSer 63
 QY 251 TGTAACTGGGAGAGAAATTTGATGAACAGCAGCTGGCGCAAGAAAACACTAGGTCAGC 310
 Db 64 PheGlnLeuGlyValGluPheaspGluValThrAlaaspArg-LysvallySer-- 82
 QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCATTAACAAT 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGATGTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
 Db 82 ----- 82
 QY 551 CGAAGACTTGTGGAGTGGTGTGGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 82 ----- 82
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGTGTCAGCA 670
 Db 83 -----valValThrLeuaspGlyGlyLysLeuValHisVa 94
 QY 671 CCAGCAATGGGAGGGAAGAGAGACGACGATAACAGAAAACCTGAAGGATGGGAAGATGAT 730
 Db 94 LGlnLysTrpAspGlyGlnGluThrThrLeuThrArgGluLeuSerAspGlyLysLeuI 114
 QY 731 CGTG 734
 Db 114 eLeu 115
 RESULT 13
 ID MYP2_BOVIN STANDARD: PRT; 131 AA.

AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80225120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine
peripheral nerve myelin.";
RL FEBS Lett. 115:27-30(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=89005045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBO J. 7:1597-1604(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=93253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic
transport proteins. Refinement of P2 myelin protein and the structure
determination and refinement of cellular retinol-binding protein in
complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
DR PIR; A03144; MPB02.
DR PDB; 1PMP; 26-JAN-95.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
FT MOD_RES 1 124
FT DISULFID 117 124
FT ACETYLATION.
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Alignment Scores:
Pred. No.: 2,41e-09 Length: 131
Score: 175.50 Matches: 51
Percent Similarity: 32.67% Conservative: 15
Best Local Similarity: 25.25% Mismatches: 26
Query Match: 7.84% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_BOVIN (1-131)

QY 131 GGAGTAGGACTGCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
DB 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProArgValIleIleSer 43

QY 191 TGTGATGCCAACATCATCGGTCAAACCCAGAGCACAGTGAAGACGACTGTGTCTCT 250
DB 44 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 63

QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACGACGCTGATGGCAGAAACACTGAGTCA 310
DB 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSerTh 83

QY 311 TACAACATACTGTGAAGCGACAGCAAGCTTCTAGATTACAGATTAATTTGCATTAACAAT 370
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QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGTATA 430
DB 88 ----- 88

QY 431 AATTAGTAAAGTCCAGGACTAAGAANYGAAGACATCTTATGAGTTCTTAGATCGAAAAA 490
DB 88 ----- 88

QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGGTGGAGTTCAGAGAGGGAAGG 550
DB 88 ----- 88

QY 551 CGAAGACTTGTGGAGTGGTGGTCTCTGGGGTCTCTTCACTTTGGAAGATGATGAAC 610
DB 88 ----- 88

QY 611 TAACTACCTCTGTATTTTTCAGACGGCTCTGCACCTTCCAAGACGGTGCCTTGGTCCAGCA 670
DB 89 -----GlySerLeuAsnGlnVa 94

QY 671 CCAGCAATGGGAGGAGACGACGATACCAAGAAAACGATGCAAGGATGGGAAGATGAT 730
DB 94 LGLnLysTrpAsnGlyAsnGluThrIleLysArgLysLeuValAspLysMetVa 114

QY 731 CGTG 734
DB 114 LVal 115

RESULT 14
FABA_HUMAN
ID FABA_HUMAN STANDARD; PRT; 131 AA.
AC P15090;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105397; PubMed=2481498;
RA Baxa C.A., Sha R.S., Buelte M.K., Smith A.J., Matarese V.,
RA Chinander L.L., Boundy K.L., Bernlohr D.A.;
RT "Human adipocyte lipid-binding protein: purification of the protein
RT and cloning of its complementary DNA.";
RL Biochemistry 28:8683-8690(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC
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CC EMBL; J02874; AA51689.1; -
DR EMBL; BC003672; AAH03672.1; -
DR PIR; A33363; A33363.
DR HSSP; P04117; 1L1D.
DR Genew; HGNC:3559; FABP4.
DR MIM; 600434; -
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;

Alignment Scores:
Pred. No.: 3,03e-09 Length: 131
Score: 174.50 Matches: 50
Percent Similarity: 32.67% Conservative: 16
Best Local Similarity: 24.75% Mismatches: 26
Query Match: 7.79% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FAB4_HUMAN (1-131)
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCACAGCTGTCATTACG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMeAlaLysProAsnMetIleIleSer 43
QY 191 TGTGTGCGCAACATCATCGGTCAAAACCGAGAGCAGACAGTGAAGACGACTGTGTCTCT 250
Db 44 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTCGGAGAGAGTGTGATGAACAGCAGCTGTGCGCAGAAAACACTGAGGTCAGC 310
Db 64 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer-- 82
QY 311 TACAACATCTGTGGAAGCGACAGAGCTTCTAGATTTCACAGATTAATAATGTCATTAACAAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAAGTACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
Db 82 ----- 82
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTTCAGACAGGCTGTCACCTTCCAAAGCGGTGCTGTCACGCA 670
Db 83 -----ThrIleThrLeuAspGlyGlyValLeuValHisVa 94
QY 671 CCAGCAATGGGAGGAGGAGCAGCAGATACAAAGAAACACTGAAGATGGGAGATGAT 730
Db 94 lGlnLysTrpAspGlyLysSerThrThrIleLysArgLysArgGluAspLysLeuVa 114
QY 731 CGTG 734
Db 114 lVal 115
RESULT 15
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FABA_MOUSE
ID FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (P2 adipocyte protein) (Myelin P2 protein
DE homolog) (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A.; Angus C.W.; Lane M.D.; Bolanowski M.A.; Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RT identification of an mRNA encoding a homologue of myelin P2
RT protein.";
RN 121 Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
RX SEQUENCE FROM N.A.
RX MEDLINE=86233319; PubMed=3520554;
RA Hunt C.R.; Ro J.H.-S.; Dobson D.E.; Min H.Y.; Spiegelman B.M.;
RT "Adipocyte P2 gene: developmental expression and homology of
RT 5'-flanking sequences among fat cell-specific genes.";
RN 133 Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
RX SEQUENCE FROM N.A.
RX MEDLINE=86278164; PubMed=3015943;
RA Phillips M.; Djan P.; Green H.;
RT "The nucleotide sequence of three genes participating in the adipose
RT differentiation of 3T3 cells.";
RN 143 J. Biol. Chem. 261:10821-10827(1986).
RX SEQUENCE.
RX MEDLINE=89008309; PubMed=2844775;
RA Matarrese V.; Bernlohr D.A.;
RT "Purification of murine adipocyte lipid-binding protein.
RT Characterization as a fatty acid- and retinoic acid-binding
RT protein.";
RN 153 J. Biol. Chem. 263:14544-14551(1988).
RX SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;
RA Arakawa T.; Hara A.; Fukunishi Y.; Konno H.; Adachi J.; Fukuda S.;
RA Aizawa K.; Izawa M.; Nishi K.; Kiyosawa H.; Kondo S.; Yamataka I.;
RA Saito T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saito R.;
RA Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.;
RA Fleischmann W.; Gaasterland T.; Glissi C.; King B.; Kochiwa H.;
RA Kuehl P.; Lewis S.; Matsuo Y.; Nikolaou I.; Pesole G.; Quackenbush J.;
RA Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Washio T.;
RA Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.;
RA Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.;
RA Brownstein M.J.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.;
RA Gustincich S.; Hill D.; Hofmann M.; Hume D.A.; Kamly M.; Lee N.H.;
RA Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.;
RA Nordone P.; Ring B.; Ringwald C.; Rodriguez I.; Sakamoto N.;
RA Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.;
RA Suzuki H.; Toyooka K.; Wang K.H.; Weitz C.; Whittaker C.; Willing L.;
RA Wynshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawai H.; Kohsaki S.;
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN 163 Nature 409:685-690(2001).
RX SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=88203618; PubMed=2452440;
RA Cook J.S.; Lucas J.J.; Sibley E.; Bolanowski M.A.; Christy R.J.;
RA Kelly T.J. Jr.; Lane M.D.;
```

"Expression of the differentiation-induced gene for fatty acid-binding protein is activated by glucocorticoid and cAMP.";
Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).

[7]
SEQUENCE OF 10-131 FROM N.A.
MEDLINE=85105214; PubMed=3968175;
Cook K.S., Hunt C.R., Spiegelman B.M.;
"Developmentally regulated mRNAs in 3T3-adipocytes: analysis of transcriptional control.";
J. Cell Biol. 100:514-520(1985).

[8]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=92207973; PubMed=1554730;
Xu Z., Bernlohr D.A., Banaszak L.J.;
"Crystal structure of recombinant murine adipocyte lipid-binding protein.";
Biochemistry 31:3484-3492(1992).

[9]
X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=93216758; PubMed=8463311;
Xu Z., Bernlohr D.A., Banaszak L.J.;
"The adipocyte lipid-binding protein at 1.6-A resolution. Crystal structures of the apoprotein and with bound saturated and unsaturated fatty acids.";
J. Biol. Chem. 268:7874-7884(1993).
-!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.

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EMBL; K02109; AAA39416.1; -
EMBL; M13264; AAA39870.1; -
EMBL; M13261; AAA39870.1; JOINED.
EMBL; M13262; AAA39870.1; JOINED.
EMBL; M13263; AAA39870.1; JOINED.
EMBL; M13385; AAA39417.1; -
EMBL; AK003143; BAB22601.1; -
EMBL; M20497; AAA37188.1; -
EMBL; M28726; AAA37112.1; -
PIR; A05089; A05089.
PIR; A24884; A24884.
PIR; A30810; A30810.
PIR; B25952; B25952.
PDB; 1ALB; 31-OCT-93.
PDB; 1LIB; 30-APR-94.
PDB; 1LIC; 30-APR-94.
PDB; 1LID; 30-APR-94.
PDB; 1LIE; 30-APR-94.
PDB; 1LIF; 30-APR-94.
PDB; 1ADL; 20-DEC-94.
PDB; 1AB0; 16-JUN-97.
PDB; 1ACD; 16-JUN-97.
PDB; 1A18; 01-JUL-98.
PDB; 1A2D; 01-JUL-98.
SWISS-2DPAGE; P04117; MOUSE.
MGD; MGI:88038; Fabp4.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation; 3D-structure.
FT INIT_MET 0 0
MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)

(BY SIMILARITY).
N -> T (IN REF. 2; AAA39870).
G -> V (IN REF. 3; AAA39417).

FT	CONFLICT	39	39	
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FT	STRAND	6	14	
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FT	TURN	24	24	
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FT	STRAND	59	64	
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FT	TURN	98	99	
FT	STRAND	100	109	
FT	TURN	110	111	
FT	STRAND	112	119	
FT	TURN	120	121	
FT	STRAND	122	130	
SQ	SEQUENCE	131 AA;	14519 MW;	ED57D4E2774B8E32 CRC64;

Alignment Scores:
Pred. No.: 3,39e-09 Length: 131
Score: 174.00 Matches: 51
Percent Similarity: 33.50% Conservative: 17
Best Local Similarity: 25.12% Mismatches: 24
Query Match: 7.77% Indels: 111
DB: 1 Gaps: 2

US-09-788-074-2 (1-1279) x FABP_MOUSE (1-131)

QY	131	GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCACG	190
Db	24	GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProsnMetIleIleSer	43
QY	191	TGIGATGGCAACAATACATACGGTCAAAACGGAGAGACAGTGAAGACGACTGTGTCTCT	250
Db	44	ValAsnGlyAspLeuValThrIleArgSerGluSerThrPhelYasnThrGluIleSer	63
QY	251	TGTAACCTGGGAGAGAGTGTGATGAACACGACAGCTGATGGCGAGAAACTGAGGTGAGC	310
Db	64	PhelYLeuGlyValGluPheAspGluIleThrAlaAspArg-LysVallyLysSer--	82
QY	311	TACAACATACTGTGAAGCGACAGAGAGCTTCTAGATTTTACAGATTAAATTGCATTAACAAT	370
Db	82	-----	82
QY	371	GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA	430
Db	82	-----	82
QY	431	AATTAGTAAAGTCCCGAGGACTAAGAAATCAAGACATCTTATCAGTTCTAGATCGAAAA	490
Db	82	-----	82
QY	491	GCACATAGTTGTATTGTGAACAAATAATCAGTATGATGGGTGGAGTTCACAGAGGGAAGG	550
Db	82	-----	82
QY	551	CGAAGACTTGTGGAGTGTGTGGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	610
Db	82	-----	82
QY	611	TAACACTCCCTGTATTTTTCAGACAGCGCTGCACCTTCCCAAGACGGTCCCTGCTCCAGCA	670
Db	83	-----IleIleThrLeuAspGlyGlyAlaLeuValGlnVa	94
QY	671	CCAGCAATGGGCGGGAAGGAGACGACGATACACAAGAAACTGAAGGATGGGAAGATGAT	730

Search completed: November 25, 2002, 10:31:46
Job time : 24 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:32 : Search time 42.5 Seconds
(without alignments)
5786.161 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 2239

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Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406.5	18.2	135	2 A47497	lipid-binding prot
2	367.5	16.4	135	2 J62201	fatty acid-binding
3	350.5	15.7	132	2 I56326	fatty acid-binding
4	200.5	9.0	132	1 MPRB2	myelin P2 protein
5	189.5	8.5	132	1 MPHU2	myelin P2 protein
6	181.5	8.1	132	2 S20297	fatty acid-binding
7	180.5	8.1	132	2 S57744	adipocyte-type fat
8	177.5	7.9	132	2 JH0407	myelin P2 protein
9	176.5	7.9	133	2 A27452	fatty acid-binding
10	175.5	7.8	131	1 MPB02	myelin P2 protein
11	174.5	7.8	132	1 F2HUF	fatty acid-binding
12	171.5	7.7	133	1 F2HUC	fatty acid-binding
13	169.5	7.6	132	2 B25952	myelin P2 protein
14	163.5	7.3	133	2 PC4011	fatty acid-binding

15	158.5	7.1	133	2 A34676	fatty acid-binding
16	155.5	6.9	132	2 A49184	fatty acid-binding
17	150.5	6.7	131	2 S06479	fatty acid-binding
18	139.5	6.2	132	2 I58161	lipid-binding prot
19	139.5	6.2	132	2 I48923	fatty acid-binding
20	136.5	6.1	132	2 I56510	fatty acid-binding
21	132.5	5.9	132	2 I52524	testis lipid bindi
22	128.5	5.7	100	2 S13796	retinoic acid-bind
23	126	5.6	136	2 T15207	hypothetical prote
24	123	5.5	95	2 A61629	retinoic acid-bind
25	121	5.4	138	2 I51265	xCRABP - African c
26	120	5.4	137	1 RJHU1	retinoic acid-bind
27	119	5.3	137	1 RJBOA	retinoic acid-bind
28	119	5.3	137	2 A35825	retinoic acid-bind
29	118	5.3	138	1 RJHU2	retinoic acid-bind
30	114	5.1	135	2 T15205	hypothetical prote
31	114	5.1	138	2 A42495	retinoic acid-bind
32	109	4.9	133	2 A39818	14K fatty acid-bin
33	106	4.7	132	2 A4864	fatty acid-binding
34	106	4.7	133	2 A48578	fatty acid-binding
35	106	4.7	134	2 S29600	fatty acid-binding
36	102	4.6	135	1 RJHU0	retinol-binding pr
37	102	4.6	135	1 RJRTO	retinol-binding pr
38	102	4.6	135	2 S16355	retinol-binding pr
39	101	4.3	839	2 T04859	extensin homolog F
40	98.5	4.4	139	2 I53298	cellular retinoic
41	98	4.4	134	2 S69360	retinol-binding pr
42	98	4.4	137	2 T25123	hypothetical prote
43	97.5	4.4	86	2 I50030	cellular retinoic
44	97.5	4.4	134	2 S43470	fatty-acid-binding
45	97.5	4.2	1522	2 T39371	transcription regu

ALIGNMENTS

RESULT 1

A47497
lipid-binding protein, keratinocyte - mouse
N:Alternate names: lipid-binding protein mall
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999
C:Accession: A47497; S36635
R:Krieg, P.; Feil, S.; Fuerstenberger, G.; Bowden, G.T.
J. Biol. Chem. 268, 17362-17369, 1993
A:Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.
A:Reference number: A47497; MUID:93352523; PMID:8349619
A:Accession: A47497
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <KRI>
A:Cross-references: EMBL:X70100; PIDN:CAA49703.1; PID:g287986
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 3.51e-32 Length: 135
Score: 406.50 Matches: 93
Percent Similarity: 45.02% Conservative: 2
Best Local Similarity: 44.08% Mismatches: 6
Query Match: 18.16% Indels: 110
DB: 2 Gaps: 1
US-09-788-074-2 (1-1279) x A47497 (1-135)

QY	131	GGAGTAGGACTGGCTTTAGGAGATGGCTGCATGGCCAGCCAGACTGTATCAGG	190
DB	27	GlyValGlyLeuAlaLeuArgLysMetAlaLaMetAlaLysProAspCysIleIleThr	46
QY	191	TCTGTGGCAACACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT	250
DB	47	CysAspGlyAsnIleThrValIysThrGluSerThrValIysThrValPheSer	66
QY	251	TGTAACCTGGGAGAGAGTTTGTGATGAACACAGCTGATGGCAGAAAAAAGCTGAGGTCAGC	310

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|||||
Db 67 CysAsnLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
QY 311 TACAACATACTGTGAGCGACACAGAGCTTCTAGATTACAGATTAAATTTGCATTACAAAT 370
Db 85 ----- 85
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAACAACTACTTTATGGAGTTGACATTTTGATA 430
Db 85 ----- 85
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
Db 85 ----- 85
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGGATTCAGAGAGGNAAGG 550
Db 85 ----- 85
QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGGGTTCCTTCTACCTTTGGAAGATGATGAAC 610
Db 85 ----- 85
QY 611 TAACCTACCTGTATTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 86 -----ValCysThrPheGlnAspGlyAlaLeuValGlnHi 97
QY 671 CCAGCAATGGAGCGGGAAGGAGCAGCAGATAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetIi 117
QY 731 CGTGGTGAGCATCAAGCACTGGCCACCATGC 761
Db 117 eValGluCysValMetAsnAlaThrCys 127

RESULT 2
JC2201
fatty acid-binding protein, cutaneous - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-2000
C:Accession: JC2201; JC7377
R:Watanabe, R.; Fujii, H.; Odani, S.; Sakakibara, J.; Yamamoto, A.; Ito, M.; Ono, T.
Biochem. Biophys. Res. Commun. 200, 253-259, 1994
A:Title: Molecular cloning of a cDNA encoding a novel fatty acid-binding protein from rat
A:Reference number: JC2201; MUID:94220094; PMID:8166694
A:Accession: JC2201
A:Molecule type: mRNA
A:Residues: 1-135 <WAT>
A:Cross-references: GB:S69874; NID:g546419; PIDN:AAB30574.1; PID:g546420
R:Odani, S.; Namba, Y.; Ishii, A.; Ono, T.; Fujii, H.
J. Biochem. 128, 355-361, 2000
A:Title: Disulfide bonds in rat cutaneous fatty acid-binding protein.
A:Reference number: JC7377
A:Contents: Skin
A:Accession: JC7377
A:Molecule type: mRNA
A:Residues: 1-135 <ODA>
C:Comment: This protein is involved in intracellular transport and metabolism of fatty acid
C:Comment: This protein, containing two disulfide bonds, is a member of intracellular,
C:Genetics:
A:Gene: c-fabp
C:Superfamily: myelin P2 protein
C:Keywords: cutaneous gland; disulfide bond; phosphoprotein; skin
F:109/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predicted
F:109/Binding site: fatty acid (Arg) #status predicted

Alignment Scores:
Pred. No.: 2,85e-28 Length: 135
Score: 367.50 Matches: 85
Percent Similarity: 43.13% Conservative: 6
Best Local Similarity: 40.28% Mismatches: 10
Query Match: 16.41% Indels: 110
DB: 2 Gaps: 1
```

```
US-09-788-074-2 (1-1279) x JC2201 (1-135)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCACTGTATCATTACG 190
Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACAACATCACGCTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCTCT 250
Db 47 LeuAspGlyAsnAsnLeuThrValLysThrGluSerThrValLysThrThrValPheSer 66
QY 251 TGTAACTGGGAGAGAAGTTTGTGAACGACAGCTGTATGGCAGAAAAAATCAGGTCAAC 310
Db 67 CysThrLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
QY 311 TACAACATACTGTGAAGCGACAGACCTTCTAGATTACAGATTAAATTTGCATTACAAAT 370
Db 85 ----- 85
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAACAACTACTTTATGGAGTTGACATTTTGATA 430
Db 85 ----- 85
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
Db 85 ----- 85
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGGATTCAGAGAGGNAAGG 550
Db 85 ----- 85
QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGGGTTCCTTCTACCTTTGGAAGATGATGAAC 610
Db 85 ----- 85
QY 611 TAACCTACCTGTATTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 86 -----ValCysThrPheThrAspGlyAlaLeuValGlnHi 97
QY 671 CCAGCAATGGAGCGGGAAGGAGCAGCAGATAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 97 sGlnLysTrpGluGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetVa 117
QY 731 CGTGGTGAGCATCAAGCACTGGCCACCATGC 761
Db 117 lValGluCysValMetAsnAlaIleCys 127

RESULT 3
I56326
fatty acid binding protein homolog - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I56326
R:Madsen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Celis, J.E.
J. Invest. Dermatol. 99, 299-305, 1992
A:Title: Molecular cloning and expression of a novel keratinocyte protein (psoriasis-
ilarity to fatty acid-binding proteins.
A:Reference number: I56326; MUID:92381332; PMID:1512466
A:Accession: I56326
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-135 <RES>
A:Cross-references: GB:M94856; NID:g182353; PIDN:AAA58467.1; PID:g182354
C:Genetics:
A:Gene: PA-FABP
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 1.44e-26 Length: 135
Score: 350.50 Matches: 78
Percent Similarity: 41.71% Conservative: 10
Best Local Similarity: 36.97% Mismatches: 13
Query Match: 15.65% Indels: 110
```

DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x I56326 (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
 Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCATCAGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTCGGAGAGAAAGTTGATGAACAGCAGCTGATGGCAGAAACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGluLysPheGluThrThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATCTCTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCGATTAAACAAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 ----- 84
 QY -431 AATTACTAAAGTCCAGGACTAAGAAATGAACACATCTTATCAGTTTCTAGATCGAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGATTGTGAACAAATPACATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTTGTGGAGTGCTGGGTCCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 84 ----- 84
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGCGGTGCGCTGGTCCAGCA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnHi 97
 QY 671 CCAGCAATGGGAGGAGAGACGACGATAACAAGAAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpaspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGACATCAAAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 4
 MPRB2
 myelin P2 protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
 C:Accession: A28081; A92266; A92372; A03145
 R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.
 J. Biol. Chem. 263, 8332-8337, 1988
 A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.
 A:Reference number: A28081; MUID:88228063; PMID:2453513
 A:Accession: A28081
 A:Molecule type: mRNA
 A:Residues: 1-132 <NAR>
 A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658
 A>Note: translation of initiator Met is not shown
 R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.
 J. Biol. Chem. 255, 1058-1063, 1980
 A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.
 A:Reference number: A92266; MUID:80094496; PMID:7356651
 A:Accession: A92266
 A:Molecule type: protein
 A:Residues: 2-56 <IS1>
 R:Ishaque, A.; Hofmann, T.; Eylar, E.H.
 J. Biol. Chem. 257, 592-595, 1982
 A:Title: The complete amino acid sequence of thr rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423
 A:Accession: A92372
 A:Molecule type: protein
 A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>
 C:Comment: P2 protein and myelin basic protein together constitute a major fraction of
 C:Superfamily: myelin P2 protein
 C:Keywords: acetylated amino end; myelin; phosphoprotein
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:20/Binding site: phosphate (Tyr) (covalent) #status predicted
 F:118-125/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 1-55e-11 Length: 132
 Score: 200.50 Matches: 55
 Percent Similarity: 35.15% Conservative: 16
 Best Local Similarity: 27.23% Mismatches: 21
 Query Match: 8.95% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPRB2 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
 Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProAsnValIleIleSer 44
 QY 191 TGTGATGGCAACATCATCAGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTCGGAGAGAAAGTTGATGAACAGCAGCTGATGGCAGAAAACTGAGGTCAGC 310
 Db 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
 QY 311 TACAACATCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCATTAAACAAT 370
 Db 83 ----- 83
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTACTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGATTGTGAACAAATPACATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTGTTCGAGTGGTGTGGGTCTCGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGCGGTGCGCTGGTCCAGCA 670
 Db 84 -----IleIleThrLeuGluArgGlyAlaLeuAsnGlnVa 95
 QY 671 CCAGCAATGGGAGGAGGAGGAGCAGCAGATAACAAGAAACTGAAGGATGGGAAGATGAT 730
 Db 95 lGlnLysTrpaspGlyLysGluThrThrIleLysArgLysLeuValAspGlyLysMetVa 115
 QY 731 CGTG 734
 Db 115 lVal 116
 RESULT 5
 MPRB2
 myelin P2 protein [validated] - human
 N:Alternate names: peripheral myelin protein 2
 C:Species: Homo sapiens (man)
 C>Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000
 C:Accession: J00977; A03143; S24224
 R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human peripheral nerve myelin; JTO977; MUID:92068191; PMID:1720307

A:Accession: JTO977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A:Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98, 'N', 100-110, 'D', 112-132 <SUZ>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction of human peripheral nerve myelin

C:Genetics:

A:Gene: GDB:PMP2

A:Cross-references: GDB:129030; OMIM:170715

A:Map position: 8q21.3-8q22.1

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2/132/Product: myelin P2 protein #status experimental <MAT>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 1,96e-10 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPH2 (1-132)

QY 131 GGAGTAGGAGTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTCAG 190

Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleLeuSer 44

QY 191 TGTGATGGCAACATCAGCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCT 250

Db 45 LysLysGlyAspIleThrIleArgThrGluSerThrPhelLysAsnThrGluIleSer 64

QY 251 TGTAACTGGGAGAGATTGTGATGAACGACAGCTGATGGCAAGAAACAGTGAAGTCA 310

Db 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83

QY 311 TACAACATACGTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAATAATTGCATTA 370

Db 83 ----- 83

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAATAAATACTTTATGGAGTTGACTTTTGATA 430

Db 83 ----- 83

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490

Db 83 ----- 83

QY 491 GCACATAGTTGTATTGTGAACAAATACATATGATGGGTGGAGTTCAGAGAGGAAAGG 550

Db 83 ----- 83

QY 551 CGAAGACTTGTGGAGTGTGGTTCCTGGGGTTCCTTCACATTTTGAAGATGATGAAC 610

Db 83 ----- 83

QY 611 TAACTACCTGTATTTTTCACAGACGGTCTGCACCTTCCAAAGACGGTGCCTCGTCAGCA 670

Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95

QY 671 CCAGCAATGGGACGGGAAGGAGACGACGATAACAAGAAACTGAAGGATGGGAAGATGAT 730

Db 95 IGINArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115

QY 731 C 731

Db 115 I 115

RESULT 6

S20297

C:Species: feline, hepatic - nurse shark

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999

C:Accession: S20297

R:Medzihradsky, K.F.; Gibson, B.W.; Kaur, S.; Yu, Z.; Medzihradsky, D.; Burlingame, Eur. J. Biochem. 203, 327-339, 1992

A:Title: The primary structure of fatty-acid-binding protein from nurse shark liver.

A:Reference number: S20297; MUID:92137215; PMID:1735421

A:Accession: S20297

A:Molecule type: protein

A:Residues: 1-132 <MED>

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; liver; phosphoprotein

F:1/Modified site: acetylated amino end (Val) #status experimental

Alignment Scores:

Pred. No.: 1,24e-09 Length: 132
Score: 181.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.11% Indels: 110
DB: 2 Gaps: 2

US-09-788-074-2 (1-1279) x S20297 (1-132)

QY 134 GTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTCAGT 193

Db 25 ValSerLeuAlaGlnArgLysValAlaThrThrValLysProLysThrIleLeuSerLeu 44

QY 194 GATGGCAACATCAGCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCTTGT 253

Db 45 AspGlyAspValIleThrIleLysThrGluSerThrPhelLysSerThrAsnIleGlnPhe 64

QY 254 AACCTGGGAGAGATTGTGATGAACGACAGCTGATGGCAAGAAACAGTGAAGTCA 313

Db 65 LysLeuAlaGluGluPheAspGluThrThrAlaAspAsnArg----- 78

QY 314 AACATACGTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAATAATTGCATTA 373

Db 78 ----- 78

QY 374 TGTACTTACTGCCAAGGGCTGACTGAAATAAATACTTTATGGAGTTGACTTTTGATAA 433

Db 79 -----ThrThrLysThrThr----- 83

QY 434 TAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 493

Db 83 ----- 83

QY 494 CATAGTTGTATTGTGAACAAATACATATGATGGGTGGAGTTCAGAGAGGAAAGCGCA 553

Db 83 ----- 83

QY 554 AGACTTGTGGAGTGTGGTTCCTGGGGTTCCTTCACATTTTGAAGATGATGAACATA 613

Db 83 ----- 83

QY 614 CTACCTGTATTTTTCACAGACGGTCTGCACCTTCCAAAGACGGTGCCTCGTCAGCACCA 673

Db 84 -----ValLysLeu-GluAsnGlyLysLeuValGlnThrGln 95

QY 674 GCAATGGGACGGGAAGGAGAGCAGCAGTAAACAAGAAACTGAAGGATGGGAAGATGATCGT 733

Db 95 mArgTrpAspGlyLysGluThrThrLeuValArgGluLeuGlnAspGlyLysLeuIleLeu 115
Qy 734 g 734
Db 115 u 115
RESULT 7
S57744
adipocyte-type fatty acid binding protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C:Accession: S57744
R:Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.
submitted to the EMBL Data Library, June 1995
A:Description: Mammary derived growth inhibitor - not a distinct protein but a mix of he
A:Reference number: S57744
A:Accession: S57744
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <SP>
A:Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 1.56e-09 Length: 132
Score: 180.50 Matches: 50
Percent Similarity: 32.18% Conservative: 15
Best Local Similarity: 24.75% Mismatches: 27
Query Match: 8.06% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x S57744 (1-132)

Qy 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProThrLeuIleLeuSer 44
Qy 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LeuAsnGlyGlyValValThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
Qy 251 TGTAACTGGGAGAGAACTTTCATGAACGACAGCTGTGGCAGAAAACTGAGTCCAC 310
Db 65 PheLysLeuGlyGlnGluPheAspGluThrProAspArg-LysValLysSer-- 83
Qy 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83
Qy 371 GTCTGTACTTACTGCCAAGGGTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
Qy 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
Qy 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGGTGAGTTTCAGAGAGGAAAGG 550
Db 83 ----- 83
Qy 551 CGAAGACTTGTGGAGTGCTGGGTCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
Qy 611 TAACTACCTGTATTTTTCACAGCGTCTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA 670
Db 84 -----IleValAsnLeuAspGluGlyAlaLeuValGlnVa 95
Qy 671 CCAGCAATGGGACGGAGGAGCAGCAGTAAACAGAAAACTGAAGGATGGGAAGATGAT 730
Db 95 IGLnAsnTrpAspGlyLysSerThrThrIleLysArgLysLeuMetAspLysMetVa 115

Qy 731 CGTG 734
Db 115 lLeu 116
RESULT 8
JH0407
myelin P2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 13-Aug-1999
C:Accession: JH0407
R:Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 75-80, 1991
A:Title: Structure of the mouse myelin P2 protein gene.
A:Reference number: JH0407; MUID:91268811; PMID:1711100
A:Accession: JH0407
A:Molecule type: DNA
A:Residues: 1-132 <NAR>
A:Cross-references: GB:S39508; NID:g232319; PIDN:AAB19249.1; PID:g232320
C:Comment: This basic protein is found in peripheral and central nervous system myel
C:Genetics:
A:Introns: 25/1; 82/3; 116/3
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 3.13e-09 Length: 132
Score: 177.50 Matches: 52
Percent Similarity: 32.23% Conservative: 16
Best Local Similarity: 24.64% Mismatches: 33
Query Match: 7.93% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x JH0407 (1-132)

Qy 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyLeuAlaAsnArgLysLeuGlyAsnLeuAlaLysProThrValIleLeuSer 44
Qy 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysLysGlyAspTyrIleThrIleArgThrGluSerAlaPheLysAsnThrGluIleSer 64
Qy 251 TGTAACTGGGAGAGAACTTTCATGAACGACAGCTGTGGCAGAAAACTGAGTCCAC 310
Db 65 PheLysLeuGlyGlnGluPheAspGluThrThrAlaAspAsnArgLysAla-LysSer-- 83
Qy 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83
Qy 371 GTCTGTACTTACTGCCAAGGGTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
Qy 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
Qy 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGGTGAGTTTCAGAGAGGAAAGG 550
Db 83 ----- 83
Qy 551 CGAAGACTTGTGGAGTGCTGGGTCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
Qy 611 TAACTACCTGTATTTTTCACAGCGTCTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA 670
Db 84 -----IleValThrLeuGluArgGlySerLeuLysGlnVa 95
Qy 671 CCAGCAATGGGACGGAGGAGCAGCAGTAAACAGAAAACTGAAGGATGGGAAGATGAT 730
Db 95 IGLnLysTrpAspGlyLysGluThrAlaIleArgArgThrLeuLeuAspGlyArgMetVa 115

QY 731 CGTGGTGAGCATCAACCACTGGCACCATGC 761
 Db 115 lValGluCysIleMetLysGlyValValCys 125

RESULT 9
 A27452
 fatty acid-binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 13-Aug-1999
 C:Accession: A28458; A27452; A28197; S06478; S02471
 R:Heuckeroth, R.O.; Birkenmeier, E.H.; Levin, M.S.; Gordon, J.I.
 J. Biol. Chem. 262, 9709-9717, 1987
 A:Title: Analysis of the tissue-specific expression, developmental regulation, and linkage of the rat fatty acid-binding protein gene
 A:Reference number: A28458; MUID:87250640; PMID:3036869
 A:Accession: A28458
 A:Molecule type: mRNA
 A:Residues: 1-133 <HEU>
 A:Cross-references: GB:J02773; NID:g204077; PIDN:AAA41136.1; PID:g204078
 A:Experimental source: cardiac
 R:Clatfey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
 Biochemistry 26, 7900-7904, 1987
 A:Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: I
 A:Reference number: A27452; MUID:88107756; PMID:3427112
 A:Accession: A27452
 A:Molecule type: mRNA
 A:Residues: 1-133 <CLA>
 A:Cross-references: GB:M18034; NID:g204079; PIDN:AAA41137.1; PID:g204080
 A:Experimental source: heart
 R:Sacchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.
 J. Biol. Chem. 261, 8218-8223, 1986
 A:Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocyte
 A:Reference number: A23838; MUID:86250713; PMID:2424895
 A:Accession: A23838
 A:Molecule type: protein
 A:Residues: 'TEKN', 5-50, 'YG', 53-64, 'N', 65-70, 'D', 72-133 <SAC>
 A:Experimental source: heart
 R:Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
 J. Biol. Chem. 266, 5963-5972, 1991
 A:Title: Primary structure and cellular distribution of two fatty acid-binding proteins
 A:Reference number: A39551; MUID:91170283; PMID:2005132
 A:Accession: A39551
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIM>
 A:Experimental source: kidney
 R:Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
 J. Biol. Chem. 263, 4182-4185, 1988
 A:Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by 1
 A:Reference number: A28197; MUID:88153733; PMID:3162235
 A:Accession: A28197
 A:Molecule type: protein
 A:Residues: 2-10; 46-53 <GTB>
 R:Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.; Mur
 Eur. J. Biochem. 185, 27-33, 1989
 A:Title: Purification and characterization of a fatty-acid-binding protein from the gast
 A:Reference number: S06478; MUID:90032682; PMID:2806260
 A:Accession: S06478
 A:Molecule type: protein
 A:Residues: 1-133 <KAN>
 A:Experimental source: stomach
 R:Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.
 Biochem. J. 251, 919-925, 1988
 A:Title: Isolation and characterization of fatty acid binding proteins from mammary tiss
 A:Reference number: S02471; MUID:88326235; PMID:3415652
 A:Accession: S02471
 A:Molecule type: protein
 A:Residues: 16-22; 32-45; 54-59, 'XX', 62-63, 'X', 65-70; 83-93; 97-107; 117-127 <JOM>
 A:Experimental source: strain Wistar; mammary
 C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
 F:1-133/Product: fatty acid-binding protein #status experimental <MAT>

F:1/Modified site: acetylated amino end (Met) #status predicted

Alignment Scores:
 Pred. No.: 3 94e-09 Length: 133
 Score: 176.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
 Best Local Similarity: 24.75% Mismatches: 26
 Query Match: 7.88% Indels: 110
 DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x A27452 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCAGACTGTATCATTCAG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
 QY 191 TGTGATGGCAACACACTACGGCTCAAAACCGAGAGACACTGAAGACGACTGTTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrIleLysThrHisSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTGGGAGAGAGTTTGTATGAACACACAGCTGATGCAGAAACACTGAGTCAGC 310
 Db 65 PheGlnLeuGlyValGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGAGACAGAGCTTCTAGATTTACAGATTAAATTCATTAACAAT 370
 Db 83 ----- 83
 QY 371 GTCGTACTTACGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTCTAGATCGAAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGTTATGCTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAGACGGTCCCTGCTCCAGCA 670
 Db 84 -----ValValThrLeuAspGlyGlyLysLeuValHisVa 95
 QY 671 CCAGCAATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 730
 Db 95 lGlnLysTrpAspGlyGlnGluThrThrLeuThrArgGluLeuSerAspGlyLysLeuI 115
 QY 731 CGTG 734
 Db 115 eLeu 116
 RESULT 10
 MBP02
 myelin P2 protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 05-Aug-1994
 C:Accession: A03144
 R:Kitamura, K.; Suzuki, M.; Umemura, K.
 FEBS Lett. 115, 27-30, 1980
 A:Title: The complete amino acid sequence of the P2 protein in bovine peripheral nerv
 A:Reference number: A03144; MUID:80225120; PMID:6156092
 A:Accession: A03144
 A:Molecule type: protein
 A:Residues: 1-131 <KIT>
 C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end
 F:1/Modified site: acetylated amino end (Ser) #status experimental
 F:117-124/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 4,96e-09 Length: 131
Score: 175.50 Matches: 51
Percent Similarity: 32.67% Conservative: 15
Best Local Similarity: 25.25% Mismatches: 26
Query Match: 7.84% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPB02 (1-131)

QY 131 GGAGTAGGACTGGCTCTTAGGAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTTACG 190
Db 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProArgValIleIleSer 43
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 44 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 63
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTAGGTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSerth 83
QY 311 TACAACATCTGTGAAGCCACAGAACTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 rValThrLeuAlaArg----- 88
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGTATA 430
Db 88 ----- 88
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 88 ----- 88
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGGGAAAGG 550
Db 88 ----- 88
QY 551 CGAAGACTGTTGGAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 88 ----- 88
QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAAGCGGTGCCCTGGTCCAGCA 670
Db 89 -----GlySerLeuAsnGlnVa 94
QY 671 CCAGCAATGGGACGGGAAGGAGCAGCAGATACAAACAACTCAAGGATGGGAAGATGAT 730
Db 94 lGlnLysTrpAsnGlyAsnGluThrThrIleLysArgLysLeuValAspGlyLysMetVa 114
QY 731 CGTG 734
Db 114 lVal 115

RESULT 11

FZHUF

fatty acid-binding protein, adipocyte - human

N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein 4
C:Species: Homo sapiens (man)
C:Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C:Accession: A33363
R:Baxa, C.A.; Sha, R.S.; Buel, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Boundy
Biochemistry 28, 8683-8690, 1989
A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloning
A:Reference number: A33363; MUID:90105397; PMID:2481498
A:Molecule type: mRNA
A:Accession: A33363

A:Residues: 1-132 <BAX>

A:Cross-references: GB:J02874; NID:q178346; PIDN:AAA51689.1; PID:q178347
A:Experimental source: subcutaneous fat

C:Genetics:

A:Gene: GDB:FABP4

A:Cross-references: GDB:128030

A:Map position: lp33-lp32

C:Superfamily: myelin P2 protein

C:Keywords: blocked amino end; lipid binding; phosphoprotein

F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #st

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Alignment Scores:

Pred. No.: 6.25e-09 Length: 132
Score: 174.50 Matches: 50
Percent Similarity: 32.67% Conservative: 16
Best Local Similarity: 24.75% Mismatches: 26
Query Match: 7.79% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FZHUF (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTAGGTCAGC 310
Db 65 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspAspArg-LysValLysSer-- 83
QY 311 TACAACATCTGTGAAGCCAGACAGAACTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGTATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTCTTGGAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAAGCGGTGCCCTGGTCCAGCA 670
Db 84 -----ThrIleThrLeuAspGlyGlyValLeuValHisVa 95
QY 671 CCAGCAATGGGACGGGAAGGAGAGCAGCAGATACAAACAACTCAAGGATGGGAAGATGAT 730
Db 95 lGlnLysTrpAspGlyLysSerThrThrIleLysArgLysGluAspAspLysLeuVa 115
QY 731 CGTG 734
Db 115 lVal 116

RESULT 12

FZHUF

fatty acid-binding protein, cardiac and skeletal muscle - human

N:Alternate names: fatty acid-binding protein 3 (FABP3)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1991 #sequence_revision 03-May-1996 #text_change 16-Jul-1999

C:Accession: S15432; JH0199; S00603; I54275; A27248

R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.

Biochem. J. 276, 203-207, 1991

A:Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protei

A:Reference number: S15432; MUID:91248148; PMID:1710107

A:Accession: S15432
A:Molecule type: mRNA; protein
A:Residues: 1-133 <PEE>
A:Cross-references: EMBL:X56549; NID:g31292; PIDN:CAA39889.1; PID:g31293
A:Experimental source: heart muscle; skeletal muscle
R:Boechers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
Mol. Cell. Biochem. 98, 127-133, 1990
A:Title: Revision of the amino acid sequence of human heart fatty acid-binding protein.
A:Reference number: JH0199; MUID:91094793; PMID:2266954
A:Accession: JH0199
A:Molecule type: protein
A:Residues: 2-129, Q', 131-133 <BOE>
R:Offner, G.D.; Brecher, P.; Sawilovich, W.B.; Costello, C.E.; Troxler, R.F.
Biochem. J. 252, 191-198, 1988
A:Title: Characterization and amino acid sequence of a fatty acid-binding protein from P.
R. Biol. Chem. 267, 18541-18550, 1992
A:Title: Three-dimensional structure of recombinant human muscle fatty acid-binding protein.
A:Reference number: A49251; MUID:92406763; PMID:1526991
A:Contents: annotation; X-ray crystallography, 2.1 angstroms
R:Note: recombinant protein expressed in *Escherichia coli*
R:Troxler, R.F.; Offner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Milunsky, A.; Wyand, J.
Hum. Genet. 92, 563-566, 1993
A:Title: Localization of the gene for human heart fatty acid binding protein to chromosome
A:Reference number: I54275; MUID:94085953; PMID:8262516
A:Accession: I54275
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 15-133 <RES>
A:Cross-references: GB:S67314; NID:g458861; PIDN:AAB29294.1; PID:g458862
C:Genetics:
A:Gene: GDB:FABP3
A:Cross-references: GDB:128008; OMIM:134651
A:Map position: lp33-lp32
C:Superfamily: myelin P2 protein
C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
F;2/Modified site: acetylated amino end (Val) (in mature form) #status experimental
F;20/Binding site: phosphate (Tyr) (covalent) #status predicted
F;127,129/Binding site: fatty acid (Arg, Tyr) #status experimental

Alignment Scores:
Pred. No.: 1 25e-08 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x F2HUC (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGACTGTCATTCACG 190
||||| ||| |||:||||:||||| |||||
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrIleIleGlu 44
QY 191 TGTGATGGCAACACATCAGCGTCAACGAGCAGACAGTGAAGACGACTGTCTCT 250
:||||: :||||: ||||| ||||| |||
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGATTGATGAACACACAGCTGATCGCAGAAAACAGGTCAGC 310
||||| :||||: ||||| ||||| |||
Db 65 PheLysLeuGlyValGluPheAspGluThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGCAGAAAGCTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGACTTATGCGCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430

QY 311 TACAACATACTGTGAAGCGCAGAGAAGCTTCTAGATTTACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAAGCTACTTTATGAGTTGATTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTCTGAACAAAATCAGATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGGTCTCGGGGGTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACACTCCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 ----- 83
QY 671 CCAGCAATGGGAGCGAAGGAGCAGCAGCAATCAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuI 115
QY 731 CGTG 734
Db 115 eLeu 116
RESULT 15
A34676
fatty acid-binding protein, cardiac - bovine
N:Alternate names: mammary-derived growth inhibitor
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 13-Aug-1999
C:Accession: A34676; S01133; A37883; A29466
R:Kurtz, A.; Vogel, F.; Funke, K.; Heldin, C.H.; Grosse, R.
J. Cell Biol. 110, 1779-1789, 1990
A:Title: Developmental regulation of mammary-derived growth inhibitor expression in bovi
A:Reference number: A34676; MUID:90243786; PMID:2335570
A:Accession: A34676
A:Molecule type: mRNA
A:Residues: 1-133 <KUR>
A:Cross-references: GB:X51933; NID:g526; PIDN:CAA36199.1; PID:g527
A:Experimental source: mammary gland
R:Billlich, S.; Wissel, T.; Kratzin, H.; Hahn, U.; Hagenhoef, B.; Lezius, A.G.; Spener, F
Eur. J. Biochem. 175, 549-556, 1988
A:Title: Cloning of a full-length complementary DNA for fatty-acid-binding protein from
A:Reference number: S01133; MUID:88312634; PMID:3409882
A:Accession: S01133
A:Molecule type: mRNA
A:Residues: 1-133 <BIL>
A:Cross-references: EMBL:X12710; NID:g338; PIDN:CAA31212.1; PID:g339
A:Experimental source: heart
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Unterberg, C.; Boerchers, T.; Hojrup, P.; Roepstorff, P.; Knudsen, J.; Spener, F.
J. Biol. Chem. 265, 16255-16261, 1990
A:Title: Cardiac fatty acid-binding proteins. Isolation and characterization of the mito
A:Reference number: A37883; MUID:90375486; PMID:2398054
A:Accession: A37883
A:Molecule type: protein
A:Residues: 2-133 <UNT>
A:Experimental source: heart
A:Note: 99-Asp was also found
R:Boehmer, F.D.; Kraft, R.; Otto, A.; Wernstedt, C.; Hellman, U.; Kurtz, A.; Mueller, T.
J. Biol. Chem. 262, 15137-15143, 1987
A:Title: Identification of a polypeptide growth inhibitor from bovine mammary gland. Seq
A:Reference number: A29466; MUID:86033096; PMID:3667628
A:Accession: A29466
A:Molecule type: protein

A:Residues: 2-12,'S',14,'E',16-40,'L',42-43,'S',45-93,'Q',95-127,'V',129-132 <BOE>
A:Experimental source: mammary gland
A:Note: 13-Asp, 94-His and 128-Thr were also found
C:Superfamily: myelin p2 protein
C:Keywords: acetylated amino end; cardiac muscle; heart; phosphoprotein
F:2-133/Product: fatty acid-binding protein, cardiac #status experimental <MAT>
F:2/Modified site: acetylated amino end (Val) (in mature form) #status experimental

Alignment Scores:
Pred. No.: 2,51e-07 Length: 133
Score: 158.50 Matches: 45
Percent similarity: 31.28% Conservative: 21
Best Local Similarity: 21.33% Mismatches: 35
Query Match: 7.08% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x A34676 (1-133)

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QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspThrValIleIleLysThrGlnSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTCATGAAACGACAGCTGATGGCAGAAAAAAGCTCAGGTCA 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGCAGAGAAGCTTCTAGATTTACAGATTAAATTCATTAACA 370
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QY 551 CGAAGACTTGTGGAGTGGTGGGTCTCGGGGGTCTTCACTTTGGAAGATGATGAAC 610
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Db 84 ----- 83
QY 671 CCAGCAATGGGAGCGAAGGAGCAGCAGCAATCAAGAACTGAAGGATGGGAAGATGAT 730
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QY 731 CGTGAGGATCAAGGACTGGGACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

Search completed: November 25, 2002, 10:33:19
Job time : 45.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:28:03 : Search time 11.5 Seconds
(without alignments)
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Title: US-09-788-074-2

Perfect score: 2239

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 200960

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PublishedApplications_AA:

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	350.5	15.7	135	US-09-788-074-3
3	189.5	8.5	132	US-09-901-436A-11
4	174.5	7.8	132	US-09-905-235-1

Alignment Scores:	5.43e-36	Length:	135
Pred. No.:	406.50	Matches:	93
Score:	45.02%	Conservative:	2
Best Local Similarity:	44.08%	Mismatches:	6
Query Match:	18.16%	Indels:	110
DB:	10	Gaps:	1

ALIGNMENTS

RESULT 1
US-09-788-074-1
; Sequence 1, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Hotamisliligil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MALL
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788, 074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-074-1

5	171.5	7.7	132	10	US-09-986-240-2	Sequence 2, Appli
6	171.5	7.7	133	10	US-09-901-436A-10	Sequence 10, Appli
7	171.5	7.7	133	12	US-10-153-740-13	Sequence 13, Appli
8	163.5	7.3	133	10	US-09-901-436A-7	Sequence 7, Appli
9	163.5	7.3	133	12	US-10-153-740-11	Sequence 11, Appli
10	158.5	7.1	133	12	US-10-153-740-12	Sequence 12, Appli
11	151.5	6.8	132	10	US-09-971-187-2	Sequence 2, Appli
12	140	6.3	131	12	US-10-153-740-15	Sequence 15, Appli
13	120	5.4	160	10	US-09-925-301-848	Sequence 328, App
14	118	5.3	138	9	US-09-736-457-328	Sequence 496, App
15	115	5.3	149	10	US-09-925-302-496	Sequence 14, Appli
16	113	5.0	156	10	US-09-737-149-14	Sequence 48, Appli
17	104	4.6	135	10	US-09-737-149-48	Sequence 2, Appli
18	104	4.6	135	12	US-10-153-740-2	Sequence 16, Appli
19	103	4.6	135	10	US-09-737-149-49	Sequence 49, Appli
20	103	4.6	135	10	US-09-901-436A-8	Sequence 8, Appli
21	102	4.6	135	10	US-09-901-436A-8	Sequence 91, Appli
22	90	3.9	598	10	US-09-853-386-91	Sequence 98, Appli
23	90	3.9	598	10	US-09-853-386-98	Sequence 2, Appli
24	89.5	3.8	3635	10	US-09-843-676-177	Sequence 177, App
25	87	3.7	153	9	US-09-864-761-37946	Sequence 37946, A
26	85.5	3.7	231	10	US-09-828-644-74	Sequence 5, Appli
27	84	3.6	1447	10	US-09-898-533-5	Sequence 1072, Ap
28	84	3.6	1447	10	US-09-901-436A-2	Sequence 2, Appli
29	82	3.5	404	10	US-09-925-301-1072	Sequence 85, Appli
30	81	3.6	107	10	US-09-745-763-85	Sequence 1393, Ap
31	80	3.4	273	10	US-09-764-864-1393	Sequence 92, Appli
32	79.5	3.4	184	10	US-09-853-386-92	Sequence 94, Appli
33	79.5	3.4	601	10	US-09-853-386-94	Sequence 46, Appli
34	79.5	3.4	601	10	US-09-737-149-46	Sequence 47, Appli
35	79	3.5	70	10	US-09-737-149-47	Sequence 2, Appli
36	79	3.5	70	10	US-09-826-508-2	Sequence 9, Appli
37	79	3.4	481	10	US-09-769-508-2	Sequence 3, Appli
38	78.5	3.5	1255	9	US-09-811-115-3	Sequence 806, App
39	78.5	3.5	1255	10	US-09-811-115-3	Sequence 2, Appli
40	78.5	3.5	1255	10	US-09-925-239-806	Sequence 434, App
41	77	3.3	271	10	US-09-858-075A-2	Sequence 17, Appli
42	77	3.3	463	10	US-09-738-973-434	Sequence 96, Appli
43	77	3.3	1702	10	US-10-104-019-17	
44	76.5	3.3	254	9	US-09-789-919-96	
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US-09-788-074-2 (1-1279) x US-09-788-074-1 (1-135)

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 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrValPheSer 66
 QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACAGACAGCTGTATGGCAGAAAACTGAGTTCAGC 310
 Db 67 CysAsnLeuGlyLysPheAspGlyLysThrAlaAspGlyArgLysThrGlu-Thr-- 85
 QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACAAT 370
 Db 85 ----- 85
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 85 ----- 85
 QY 431 AATTAGTAAAGTCCAGAGCTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
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 Db 85 ----- 85
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 Db 86 -----ValCysThrPheGlnAspGlyAlaLeuValGlnhi 97
 QY 671 CCAGCAATGGGCGGAGGAGGAGCAGCAGATACAGAAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetIi 117
 QY 731 CGTGTGTGACATCAAGCACTGGCCACCATGC 761
 Db 117 eValGluCysValMetAsnAlaThrCys 127

RESULT 2

US-09-788-074-3
 ; Sequence 3, Application US/09788074
 ; Patent No. US20010044110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotamisligil, Gokhan S.
 ; TITLE OF INVENTION: INHIBITION OF MAL1
 ; FILE REFERENCE: 21509-044
 ; CURRENT APPLICATION NUMBER: US/09/788,074
 ; CURRENT FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,106
 ; PRIOR FILING DATE: 2000-02-17
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-788-074-3

Alignment Scores:
 Pred. No.: 6.34e-30 Length: 135
 Score: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-788-074-3 (1-135)

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 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
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 QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACAGACAGCTGTATGGCAGAAAACTGAGTTCAGC 310
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 QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACAAT 370
 Db 84 ----- 84
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 Db 84 ----- 84
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 QY 611 TAACTACCTGTATTTTGCAGACGGTCTGCACCTTCCAAAGCGTGCCTCGTCACAGA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnhi 97
 QY 671 CCAGCAATGGGCGGAGGAGGAGCAGCAGATACAGAAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGTGACATCAAGCACTGGCCACCATGC 761
 Db 117 iValGluCysValMetAsnValThrCys 127

RESULT 3

US-09-901-436A-11
 ; Sequence 11, Application US/09901436A
 ; Patent No. US20020098515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI et al.
 ; TITLE OF INVENTION: Cytostatin I
 ; FILE REFERENCE: PFI75D4
 ; CURRENT APPLICATION NUMBER: US/09/901,436A
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 09/361,737
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: 09/023,073
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 08/470,298
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: 08/409,731
 ; PRIOR FILING DATE: 1995-03-24
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-901-436A-11

Alignment Scores:
 Pred. No.: 1.74e-12 Length: 132
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservative: 16
 Best Local Similarity: 26.37% Mismatches: 22
 Query Match: 8.46% Indels: 110
 Db: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-901-436A-11 (1-132)

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 DB 45 LysLysGlyAspIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTGGGAGAGAAAGTTTCATGAACAGCAGCTGATGGCAGAAAACAGTGCAGC 310
 DB 65 PheLysLeuGlyGlnGluPheGluGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
 DB 83 ----- 83
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 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
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 DB 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
 QY 671 CCAGCAATGGGACGAGGAGCAGCAGTAAACAAGAACTGAAGAGTGGGAAGATGAT 730
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RESULT 4
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 ; Sequence 1, Application US/09905235
 ; Patent No. US20020035064A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 ; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND COMBI
 ; FILE REFERENCE: LA24a
 ; CURRENT APPLICATION NUMBER: US/09/905.235
 ; CURRENT FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-905-235-1

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Pred. No.: 7.36e-11 Length: 132
 Score: 174.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
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 Query Match: 7.79% Indels: 110
 Db: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-905-235-1 (1-132)

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 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGACGACAGTGAAGACGACTGTGTCTCT 250
 DB 45 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTGGGAGAGAAAGTTTCATGAACAGCAGCTGATGGCAGAAAACAGTGCAGC 310
 DB 65 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
 DB 83 ----- 83
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 DB 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 DB 83 ----- 83
 QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGAGTTTCAGAGAGGAAAGG 550
 DB 83 ----- 83
 QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 DB 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACAGCGTGTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
 DB 84 -----ThrIleThrLeuAspGlyValLeuValHisVa 95
 QY 671 CCAGCAATGGGACGAGGAGCAGCAGTAAACAAGAACTGAAGAGTGGGAAGATGAT 730
 DB 95 IGlNArgTrpaspGlyLysSerThrThrIleLysArgLysArgGluAspAspLysLeuVa 115
 QY 731 C 731
 DB 115 I 115

RESULT 5
 US-09-986-240-2
 ; Sequence 2, Application US/09986240
 ; Patent No. US20020119496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weigelt, Johan
 ; APPLICANT: Wilström, Mats
 ; TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
 ; FILE REFERENCE: 13425-047001
 ; CURRENT APPLICATION NUMBER: US/09/986,240
 ; CURRENT FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: 60/243,626
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: SE 0003811-7
 ; PRIOR FILING DATE: 2000-10-20
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 132

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-240-2

Alignment Scores:
Pred. No.: 1,56e-10 Length: 132
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-986-240-2 (1-132)

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Db 24 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 43
QY 191 TGTGATGGCAACAATCATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 44 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelysAsnThrGlulleSer 63
QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACAGCTGATGGCAGAAAACACTGAGGTGACG 310
Db 64 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 82
QY 311 TACAACATACCTGTGAAGCGCACAGAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 82 ----- 82
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACATACCTGTATTTTGCACACGGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 83 ----- 83
QY 671 CCAGCAATGGGAGCGGAGGAGCAGACGATGAAGAACTGAAGGATGGAAGATGAT 730
Db 94 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 114
QY 731 CGTGGTGAGCATCAAGACACTGGCACCATGC 761
Db 114 eLeuThrLeuThrHisGlyThrAlaValCys 124
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RESULT 6

US-09-901-436A-10
; Sequence 10, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PFI75D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298

; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-10

Alignment Scores:

Pred. No.: 1,56e-10 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-901-436A-10 (1-133)

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QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACAATCATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelysAsnThrGlulleSer 64
QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACAGCTGATGGCAGAAAACACTGAGGTGACG 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACCTGTGAAGCGCACAGAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACATACCTGTATTTTGCACACGGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 84 ----- 84
QY 671 CCAGCAATGGGAGCGGAGGAGCAGACGATGAAGAACTGAAGGATGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 115
QY 731 CGTGGTGAGCATCAAGACACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
```

RESULT 7

US-10-153-740-13
; Sequence 13, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.

;; DILLON, PATRICK
;; TITLE OF INVENTION: CYTOSTATIN III
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MD
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/153,740
;; FILING DATE: 24-May-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/734,036
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 09/307,817
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROOKES, ANDERS A.
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PF222
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 133 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-153-740-13

Alignment Scores:
Pred. No.: 1,56e-10 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-13 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATATTACG 190
Db 25 GlyValGlyPheAlaThrArgInValAlaSerMetThrLysProThrThrIlelleGlu 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCCGAGACAGCAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAAGAAAACACTGAGGTTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCACAGATTAAATTTGCATTAAACAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490

Db 83 ----- 83
QY 491 GCACATAGTTGATTGTAACAAAATACGTATGATGGGTGGGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGGGTTCCTTCACTTTTGGAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCCTGTATTTTTCAGACAGCTGTGCACCTTCCAAGACGGTGCCTGTTCAGCA 670
Db 84 -----IleValThrLeuAspGlyGlyLysLeuValHisLe 95
QY 671 CCAGCAATGGGACGGGAAGAGAGACGACGATACAAAGAAAACCTGAAGGATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 115
QY 731 CGTGGTGAGCATCAAGACACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 8
US-09-901-436A-7
; Sequence 7, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF17504
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO: 7
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-7
Alignment Scores:
Pred. No.: 1.15e-09 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 10 Gaps: 1
US-09-788-074-2 (1-1279) x US-09-901-436A-7 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATATTACG 190
Db 25 GlyValGlyPheAlaThrArgInValAlaSerMetThrLysProThrThrIlelleGlu 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAAGAAAACACTGAGGTTCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCACAGATTAAATTTGCATTAAACAT 370
Db 83 ----- 83

```
;
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-153-740-11

Alignment Scores:
Pred. No.: 1.15e-09 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-11 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCCAAGCCAGACTGTATCATTAGC 190
Db 25 GYVAlGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGCCAACAAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPhelYsAsnThrGluIleAsn 64
QY 251 TCTAACCTGGGAGAGAAGTTTGATGAACAGCACAGCTGATGGCAGAAAAAAGTCAAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATCTCTGAAGCCAGAGAGACCTTCTAGATTACAGATTAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGNACAAAATCAGTATCATGGGTGGAGTTCAGAGAGGNAAG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CCAGCAATGGGACGGGAAGGAGAGACGATGAACAAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuIle 115
QY 731 CGTG 734
Db 115 eLeu 116

RESULT 9
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-153-740-11

Alignment Scores:
Pred. No.: 1.15e-09 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-11 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCCAAGCCAGACTGTATCATTAGC 190
Db 25 GYVAlGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGCCAACAAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPhelYsAsnThrGluIleAsn 64
QY 251 TCTAACCTGGGAGAGAAGTTTGATGAACAGCACAGCTGATGGCAGAAAAAAGTCAAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATCTCTGAAGCCAGAGAGACCTTCTAGATTACAGATTAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGNACAAAATCAGTATCATGGGTGGAGTTCAGAGAGGNAAG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CCAGCAATGGGACGGGAAGGAGAGACGATGAACAAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuIle 115
QY 731 CGTG 734
Db 115 eLeu 116

RESULT 10
US-10-153-740-12
; Sequence 12, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
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CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,740
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/734,036
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/307,817
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-740-12

Alignment Scores:
Pred. No.: 4e-09 Length: 133
Score: 158.50 Matches: 45
Percent Similarity: 31.28% Conservative: 21
Best Local Similarity: 21.33% Mismatches: 35
Query Match: 7.08% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-12 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGACAGCTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspThrValIleIleLysThrGlnSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTCAGATTAAATTGCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAG 550
Db 83 ----- 83

QY 551 CGAAGACTTGTGGAGTGGTGTGGGTCCCTGGGGGTTCTTCCTTCTTGGAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTATTTTGCAGACAGGTGTGCACCTTCCAAGACGGTGCCCTGTGTCCAGCA 670
Db 84 -----IleValThrLeuAspGlyGlyLysLeuValHisVa 95
QY 671 CCAGCAATGGGAGGGAAGAGAGACGACGATACAAAGAACTGAAGATGGGGAAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrSerLeuValArgGluMetValAspGlyLysLeuIl 115
QY 731 CGTGGTGAGCATCAAAAGCAGCTGCCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
; Patent No. US20020031804A1
; GENERAL INFORMATION:
; APPLICANT: Jian Ni et al.
; TITLE OF INVENTION: Cytostatin II
; FILE REFERENCE: PF221D1
; CURRENT APPLICATION NUMBER: US/09/971,187
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/043,646
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/US95/12540
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: human
US-09-971-187-2
Alignment Scores:
Pred. No.: 2.29e-08 Length: 132
Score: 151.50 Matches: 48
Percent Similarity: 32.51% Conservative: 18
Best Local Similarity: 23.65% Mismatches: 25
Query Match: 6.77% Indels: 112
DB: 10 Gaps: 4
US-09-788-074-2 (1-1279) x US-09-971-187-2 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGACAGCTGAAGACGACTGTGTCTCT 250
Db 45 GlnGluGlyAspLysValValIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 65 PheGlnLeuGlyGluGluPheAspGluThrThrAlaAspArg----- 79
QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTCAGATTAAATTGCATTAACAAT 370
Db 80 -----AsnCys----- 81
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATCTACTTTATGGAGTTGACTTTTGATA 430
Db 81 ----- 81
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
Db 82 -----Lys 82
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAG 550

Db 83 Ser-ValValSerLeu----- 87
QY 551 CGAAGACTTGTGGAGTGTGGTCTCGGGGTTCTTCACTTTTGAAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACTACCTGTATTTTTCAGAGCGGTCTGCACCTTCCAAAGCGGT---GCCCTGGTCCA 667
Db 88 -----AspGlyAspLysLeuValHi 94
QY 668 GCACCAGCAATGGACGGGGAAGAGACGACGATACAAAGAACTGAAGATGGGAGAT 727
Db 94 sileGlnLysTrpAspGlyLysGluThrAsnPheValArgGluIleLysAspGlyLysMe 114
QY 728 GATCGTG 734
Db 114 tValMet 116
RESULT 12
US-10-153-740-15
; Sequence 15, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-153-740-15
Alignment Scores:
Pred. No.: 4 01e-07 Length: 131
Score: 140.00 Matches: 48
Percent Similarity: 32.02% Conservatives: 17
Best Local Similarity: 23.65% Mismatches: 25

Query Match: 6.25% Indels: 113
DB: 12 Gaps: 5
US-09-788-074-2 (1-1279) x US-10-153-740-15 (1-131)
QY 131 GGAGTAGGACTGCTCTTTAGGAAGATGGCTGCATATGCCAAGCCAGACTGATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACAACATCACGGTCAAACCCGAGAGACAGCTGAAGACGACTGTGTTCTCT 250
Db 45 GlnGluGlyAspLysValIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACACAGCTGTGTCGCAAAAACTGAGTCAAGC 310
Db 65 PheGlnLeuGlyGlu---PheAspGluThrThrAlaAspAspArg----- 78
QY 311 TACAACATACTGTGAAGCCGACAGAACGTTCTAGATTTACAGATTAATTCATTAACAAT 370
Db 79 -----AsnCys----- 80
QY 371 GTCGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 80 ----- 80
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAACACATCTTATGAGTTCTAGATCGAAAA 490
Db 81 -----Lys 81
QY 491 GCACATAGTTGTATTGTGAACAAATACGATATGATGGGTGGAGTTTCAGAGAGGAAAG 550
Db 82 Ser-ValValSerLeu----- 86
QY 551 CGAAGACTTGTGGAGTGTGGTCTCGGGGTTCTTCACTTTTGAAGATGATGAAC 610
Db 86 ----- 86
QY 611 TAACTACCTGTATTTTTCAGAGCGGTCTGCACCTTCCAAAGACGGT---GCCCTGGTCCA 667
Db 87 -----AspGlyAspLysLeuValHi 93
QY 668 GCACCAGCAATGGACGGGGAAGAGACGACGATACAAAGAACTGAAGATGGGAGAT 727
Db 93 sileGlnLysTrpAspGlyLysGluThrAsnPheValArgGluIleLysAspGlyLysMe 113
QY 728 GATCGTG 734
Db 113 tValMet 115
RESULT 13
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-848

Alignment Scores:

Pred. No.: 6,39e-05 Length: 160
 Score: 120.00 Matches: 30
 Percent Similarity: 60.61% Conservative: 10
 Best Local Similarity: 45.45% Mismatches: 23
 Query Match: 5.36% Indels: 3
 DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-925-301-848 (1-160)

QY 131 GGAGTAGGACTGGCTCTTAGGAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
 Db 47 GlyValAsnAlaMetLeuArgLysValAlaValAlaAlaSerLysProHisValGlu 66
 QY 185 ATTACGTGTGATGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
 Db 67 IleArgGlnAspGlyAspGlnPheThrSerThrThrValArgThrThrGlu 86
 QY 245 TTCTCTTTAACTGGGAGAGTGTGATGAACGACAGCTGATGGCAGAAAAAAGTGTAG 304
 Db 87 IleAsnPheLysValGlyGluGluPheGluGluThrValAspGlyArg-LysCysSar 106
 QY 305 GTCAGCTACACATAC 320
 Db 106 gSerLeuAlaThrTrp 111

RESULT 14

US-09-736-457-328

; Sequence 328, Application US/09736457

; Patent No. US20020168637A1

; GENERAL INFORMATION:

; APPLICANT: Wang, TongLong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Lique

; APPLICANT: Wang, Aljun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736,457

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 328

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-736-457-328

Alignment Scores:

Pred. No.: 9,92e-05 Length: 138
 Score: 118.00 Matches: 28
 Percent Similarity: 61.04% Conservative: 19
 Best Local Similarity: 36.36% Mismatches: 22
 Query Match: 5.27% Indels: 8
 DB: 9 Gaps: 2

US-09-788-074-2 (1-1279) x US-09-736-457-328 (1-138)

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 Db 10 IleIleArgSerGluAsnPheGluGluLeuLeuLysVal-----Leu 23
 QY 131 GGAGTAGGACTGGCTCTTAGGAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
 Db 24 GlyValAsnValMetLeuArgLysIleAlaValAlaAlaSerLysProAlaValGlu 43

QY 185 ATTACGTGTGATGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
 Db 44 IleLysGlnGluGlyAspThrPheThrIleLysThrSerThrValArgThrThrGlu 63
 QY 245 TTCTCTTTAACTGGGAGAGAGTGTGATGAACGACAGCTGTATGGCAGA 295
 Db 64 IleAsnPheLysValGlyGluGluPheGluGluThrValAspGlyArg 80
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 ; Sequence 496, Application US/09925302
 ; Patent No. US20020044941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA104
 ; CURRENT APPLICATION NUMBER: US/09/925,302
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 896
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 496
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-302-496
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 Score: 118.00 Matches: 28
 Percent Similarity: 61.04% Conservative: 19
 Best Local Similarity: 36.36% Mismatches: 22
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 DB: 10 Gaps: 2

US-09-788-074-2 (1-1279) x US-09-925-302-496 (1-149)

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 Db 21 IleIleArgSerGluAsnPheGluGluLeuLeuLysVal-----Leu 34
 QY 131 GGAGTAGGACTGGCTCTTAGGAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
 Db 35 GlyValAsnValMetLeuArgLysIleAlaValAlaAlaSerLysProAlaValGlu 54
 QY 185 ATTACGTGTGATGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
 Db 55 IleLysGlnGluGlyAspThrPheThrIleLysThrSerThrValArgThrThrGlu 74
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Search completed: November 25, 2002, 10:34:31

Job time : 15.5 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:53 ; Search time 17.5 Seconds
(without alignments)
4300.791 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 2339

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Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	350.5	15.7	135	1	US-08-446-600A-4 Sequence 4, Appli
2	189.5	8.5	132	1	US-08-409-731A-11 Sequence 11, Appl
3	189.5	8.5	132	2	US-08-470-298B-11 Sequence 11, Appl
4	189.5	8.5	132	2	US-09-023-073A-11 Sequence 11, Appl
5	189.5	8.5	132	4	US-09-361-737-11 Sequence 11, Appl
6	171.5	7.7	133	1	US-08-409-731A-10 Sequence 10, Appl
7	171.5	7.7	133	2	US-08-470-298B-10 Sequence 10, Appl
8	171.5	7.7	133	2	US-08-820-825-13 Sequence 10, Appl
9	171.5	7.7	133	2	US-09-023-073A-10 Sequence 10, Appl
10	171.5	7.7	133	4	US-09-307-817-13 Sequence 13, Appl
11	171.5	7.7	133	4	US-09-361-737-10 Sequence 10, Appl
12	171.5	7.7	133	4	US-09-734-036-13 Sequence 11, Appl

13	163.5	7.3	131	1	US-08-409-731A-7	Sequence 7, Appli
14	163.5	7.3	131	2	US-08-470-298B-7	Sequence 7, Appli
15	163.5	7.3	133	2	US-08-820-825-11	Sequence 11, Appl
16	163.5	7.3	133	4	US-09-023-073A-7	Sequence 7, Appli
17	163.5	7.3	133	4	US-09-307-817-11	Sequence 11, Appl
18	163.5	7.3	133	4	US-09-361-737-7	Sequence 7, Appli
19	163.5	7.3	133	4	US-09-734-036-11	Sequence 11, Appl
20	158.5	7.1	133	2	US-08-820-825-12	Sequence 12, Appl
21	158.5	7.1	133	4	US-09-307-817-12	Sequence 12, Appl
22	158.5	7.1	133	4	US-09-734-036-12	Sequence 12, Appl
23	151.5	6.8	132	4	US-09-043-646-2	Sequence 2, Appli
24	140	6.3	131	2	US-08-820-825-15	Sequence 15, Appl
25	140	6.3	131	4	US-09-307-817-15	Sequence 15, Appl
26	140	6.3	131	4	US-09-734-036-15	Sequence 15, Appl
27	139.5	6.2	132	4	US-08-470-298B-12	Sequence 12, Appl
28	120	5.4	137	1	US-08-468-709B-4	Sequence 4, Appli
29	120	5.4	137	2	US-08-241-664B-4	Sequence 4, Appli
30	120	5.4	137	5	PCT-US93-03936-4	Sequence 4, Appli
31	119	5.3	137	1	US-08-468-709B-11	Sequence 11, Appl
32	119	5.3	137	2	US-08-241-664B-11	Sequence 11, Appl
33	118	5.3	138	1	US-08-468-709B-2	Sequence 2, Appli
34	118	5.3	138	2	US-08-241-664B-2	Sequence 2, Appli
35	118	5.3	138	5	PCT-US93-03936-2	Sequence 2, Appli
36	109	4.9	133	1	US-08-554-463-1	Sequence 1, Appli
37	108	4.8	138	1	US-08-468-709B-12	Sequence 12, Appl
38	108	4.8	138	2	US-08-241-664B-12	Sequence 12, Appl
39	104	4.6	135	2	US-08-820-825-2	Sequence 2, Appli
40	104	4.6	135	4	US-09-307-817-2	Sequence 2, Appli
41	104	4.6	135	4	US-09-734-036-2	Sequence 2, Appli
42	102	4.6	135	1	US-08-409-731A-8	Sequence 8, Appli
43	102	4.6	135	2	US-08-470-298B-8	Sequence 8, Appli
44	102	4.6	135	2	US-08-847-724-4	Sequence 4, Appli
45	102	4.6	135	2	US-08-847-724-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: No. 5719126dlund, James J. and Farooqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frost & Jacobs
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
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; TELEX: 21-4396 F&J Cin
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
US-08-446-600A-4

Alignment Scores:
Pred. No.: 1,14e-32 Length: 135
Score: 350.50 Matches: 78
Percent Similarity: 41.71% Conservative: 10
Best Local Similarity: 36.97% Mismatches: 13
Query Match: 15.65% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-446-600A-4 (1-135)
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QY 191 TGTGATGGCAACATACAGCTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAGAAACAACTGAGTCAAGC 310
Db 67 CysThrLeuGlyGluLysPheGluThrThrAlaAspGlyArgLysThr-Gln----- 84
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTTCACAGATTAAATTCGATTAAACAAT 370
Db 84 ----- 84
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
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QY 611 TAACTACCTGTATTTTTCACAGCGTCTGCACCTTCCAAAGCGTGCCTGGTCCAGCA 670
Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnH1 97
QY 671 CCAGCAATGGGAGGAGGAGCAGCAGTAAACAGAAACTGAAGGATGGGAAGATGAT 730
Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
QY 731 CGTGGTGCACATCAAGACACTGGCACCATGC 761
Db 117 iValGluCysValMetAsnAsnValThrCys 127

RESULT 2
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,731A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PE175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-409-731A-11

Alignment Scores:
Pred. No.: 1.02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-409-731A-11 (1-132)
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Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACATACATCAGCTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAGAAACAACTGAGTCAAGC 310
Db 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTTCACAGATTAAATTCGATTAAACAAT 370
Db 83 ----- 83
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QY 731 C 731
Db 115 I 115

RESULT 3
US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
US-08-470-298B-11

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Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-470-298B-11 (1-132)
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QY 251 TCTAACTCTGGGAGAGAAAGTTTGATGAAACGACAGCTGTGGCAGAAAAAACTGAGGTCAC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrThrIleAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACACTACTGTGAAGCGACAGAAAGCTTCTAGATTTCACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCCGAGCACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
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QY 671 CCAGCAATGGGACGGAGGAGGACGATACACAGAACTGAAGACTGGGAAGATGAT 730
Db 95 lGlnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 C 731
Db 115 I 115

RESULT 4
US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43, 975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
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; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-023-073A-11

Alignment Scores:
Pred. No.: 1 02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservatives: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 2 Gaps: 1

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QY 191 TGTGATGGCAACAATCATCGGTCAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPhelYsAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAACTGAGTGCAGC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAACTCTAGATTTACAGATTAATAATGCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGCTGGAGTTCACAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGGTCCTGGGGGTTCCCTTCACTTTTGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAAAGCGGTGCCTGGTCAGCA 670
Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGCGGAGGAGGACGATAAACAAGAAACTGAAGGATGGGAAGATGAT 730
Db 95 IGLNArgTrpaspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 C 731
Db 115 1 115

RESULT 5
US-09-361-737-11
; Sequence 11, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
```


Qy 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAGCCAGACTGTATCATTAGC 190

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: FABP (FIGURE 2)
ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-470-298B-10 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACATCAGGTCAAACCGAGACAGACAGTGAAGCAGTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelYsAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAAGAACTAGGTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-Lysvallysser-- 83
QY 311 TACAACATCTGTGAAGCGACAGAACTTCTAGATTTACAGATTAATAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGAGCGTCCCTGTCCAGCA 670
Db 84 ----- 83
QY 671 CCAGCAATGGGCGGAGGAGACAGTATACAGAAATACTGAAGGATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle 115
QY 731 CGTGGTGAGCATCAAGAGCTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 8
US-08-820-825-13
Sequence 13, Application US/08820825
Patent No. 5945309
GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-820-825-13

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-820-825-13 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACATCAGGTCAAACCGAGACAGACAGTGAAGCAGTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelYsAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAAGAACTAGGTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-Lysvallysser-- 83
QY 311 TACAACATCTGTGAAGCGACAGAACTTCTAGATTTACAGATTAATAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTTATTGTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAG 550

Db	83	-----	83
Qy	551	CGAAGACTTGTTGGAGTGGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC	610
Db	83	-----	83
Qy	611	TAACTACCCTGTATTTTTCAGACAGCTGTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA	670
Db	84	-----IleValThrLeuAspGlyGlyLeuValHisLe	95
Qy	671	CCAGCAATGGGACGGGAAGGAGACACGATAACACAAACACTGAAGCATGGGAAGATGAT	730
Db	95	uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI	115
Qy	731	CGTGGTGAGCATCAAGCACTGGCCACCATGC	761
Db	115	eLeuThrLeuThrHisGlyThrAlaValCys	125

```

RESULT 9
US-09-023-073A-10
; Sequence 10, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; -APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; *NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA

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1  ZIP: 20630
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: PatentIn Release #1.0, Version #1.30
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/023,073A
9  FILING DATE: 13-FEB-1998
10 CLASSIFICATION: 424
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Wales, Michele M.
13 REGISTRATION NUMBER: P-43, 975
14 REFERENCE/DOCKET NUMBER: PF175D2
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 301-610-5772
17 TELEFAX: 301-309-8439
18 INFORMATION FOR SEQ ID NO: 10:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 133 amino acids
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: protein
25 US-09-023-073A-10

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Alignment Scores:		
Pred. No.:	1,35e-11	Length:
Score:	171.50	Matches:
Percent Similarity:	32.23%	Conservative:
Best Local Similarity:	23.70%	Mismatches:
Query Match:	7.66%	Indels:
DB:	2	Gaps:
		133
		50
		18
		33
		110
		1

US-09-788-074-2 (1-1279) x US-09-023-073A-10 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATACG 190

Db	25	GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrIleLeuGlu	44
Qy	191	TGTCATGGCAACATCATCGGTCAAAACCGAGACACAGTGAAGACGACTGTGTTCTCT	250
Db	45	LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPheLysAsnThrGluIleSer	64
Qy	251	TGTAACCTGGGAGAGAAGTTTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTCCAG	310
Db	65	PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer	83
Qy	311	TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAATTCGATTAAACAAT	370
Db	83	-----	83
Qy	371	GTCTGTACTTACTGCCAAGGGCTACTGAAAAAACAATCTTTATGGAGTTGCATTTTGATA	430
Db	83	-----	83
Qy	431	AATTAGTAAAGTCCCAAGGACTAAGAAATGAACACATCTTATCAGTTTCTAGATCGAAAA	490
Db	83	-----	83
Qy	491	GCACATAGTTGTATTGTGAACAAAATCAGTATCATGGGTGGAGTTCAGAGAGGGAAGG	550
Db	83	-----	83
Qy	551	CGAAGACTTGTGGAGTGGTGGTGCTGGGGTCTTCACTTTGGAAGATGATGAAC	610
Db	83	-----	83
Qy	611	TAACACCTGTATTTTTCAGACGCTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA	670
Db	84	-----lLeValThrLeuAspGlyGlyLysLeuValHisLe	95
Qy	671	CCACATGGGACGGGAAGAGACGACGATGAACAGAAAACTCAAGATGGGAAGATGAT	730
Db	95	uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle	115
Qy	731	CGTGGTCGAGCATCAAGCACTGGCCACCATGC	761
Db	115	eLeuThrLeuThrHisGlyThrAlaValCys	125
RESULT 10			
US-09-307-817-13			
; Sequence 13, Application US/09307817			
; Patent No. 6232291			
; GENERAL INFORMATION:			
; APPLICANT: NI, JIAN			
; APPLICANT: YU, GUO-LIANG			
; APPLICANT: GENTZ, REINER L.			
; APPLICANT: DILLON, PATRICK			
; TITLE OF INVENTION: CYTOSTATIN III			
; NUMBER OF SEQUENCES: 15			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.			
; STREET: 9410 KEY WEST AVENUE			
; CITY: ROCKVILLE			
; STATE: MD			
; COUNTRY: USA			
; ZIP: 20850			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/307,817			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/820,825			
; FILING DATE:			

ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PE222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-307-817-13

Alignment Scores:
Pred. No.: 1.35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-307-817-13 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
DB 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
DB 45 LysAsnGlyAspIleLeuThrLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAACTGAGGTACGC 310
DB 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATAGTGTGAAGCGCACAGAGCTTCTAGATTACAGATTAAATTCATTACAAT 370
DB 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAATGAACACATCTTATCAGTTCTAGATCGAAAA 490
DB 83 ----- 83
QY 491 GCATAGTATTGTATGTAACAAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
DB 83 ----- 83
QY 551 CGAAGACTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
DB 83 ----- 83
QY 611 TACTACCTGTATTTTGCAGACGGTCTGCACCTTCCAAAGACGGTGCCTGTCAGCA 670
DB 84 -----fLeValThrLeuAspGlyGlyLysLeuValHisLe 95
QY 671 CCAGCAATGGAGGAGGACGACGATGAACAAGAAACTGAGGATGGGAAGATGAT 730
DB 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle 115
QY 731 CGTGGTGAGCATCAAAAGCACTGGCACCATGC 761
DB 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 11
US-09-361-737-10
Sequence 10, Application US/09361737

Patent No. 6287812
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-361-737-10

Alignment Scores:
Pred. No.: 1.35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-361-737-10 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
DB 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
DB 45 LysAsnGlyAspIleLeuThrLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAACTGAGGTACGC 310
DB 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATAGTGTGAAGCGCACAGAGCTTCTAGATTACAGATTAAATTCATTACAAT 370
DB 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 83 ----- 83

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTCTGAACAAATCACTATCATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTTGGAGTGTGTGGTCCCGGGGTTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 84 -----11eValThrLeuAspGlyGlyLeuValHisLe 95
QY 671 CCAGCAATGGGAGGAGGAGCAGCATAACAGAAAACTGAAGCATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 115
QY 731 CGTGGTGAGCATCAAGCACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 12

US-09-734-036-13
; Sequence 13, Application US/09734036
; Patent No. 6413726
; GENERAL INFORMATION:
; *APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09734,036
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,817
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-734-036-13

Alignment Scores: 1.35e-11 Length: 133
Pred. No.: 171.50 Matches: 50
Score:

Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1
US-09-788-074-2 (1-1279) x US-09-734-036-13 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGGTGCCATGCCAAGCCAGACTGTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTCTGGGAGAGAAGTTTGTATGAACGACACAGCTGTGGCAGAAAACTGAGGTCCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysvalLysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGTGCCTGACTGAAAAAACTACTTTATGGAGTTGCATTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATCAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTTGTGGAGTGTGTGGTCCCTGGGGGTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----11eValThrLeuAspGlyGlyLeuValHisLe 95
QY 671 CCAGCAATGGGAGGAGGAGCAGCAGCAGTAAACAGAAAACTGAAGCATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 115
QY 731 CGTGGTGAGCATCAAGCACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 13

US-08-409-731A-7
; Sequence 7, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/409,731A
 FILING DATE: 24-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Robert H
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PF175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8512
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-409-731A-7

Alignment Scores:
 Pred. No.: 1.17e-10 Length: 131
 Score: 163.50 Matches: 46
 Percent Similarity: 33.17% Conservative: 21
 Best Local Similarity: 22.77% Mismatches: 25
 Query Match: 7.30% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-409-731A-7 (1-131)

QY 131 GGAGTAGGACTGGCTTATAGGAAGATGGCTGCATGCCAAGCCAGACTGTATCATTACG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
 QY 191 TGTGATGGAACAACATACGCTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
 QY 251 TGTAACTGGGAGAGAGTGTATGTAACACGACAGCTGTGGCAGAAACACTGAGTCA 310
 Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACA 370
 Db 83 ----- 83
 QY 371 GTCTGTACTACTGCCAAGGGCTGACTGAAATAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACCTAAGAAATGAAGACATCTTATCAGTTTCTAGATCGAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGTATTGTGAACAAATACATGATGATGGGTGGGTTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTCCCTGTCCAGCA 670
 Db 84 -----LeuValThrLeuAspGlyLysLeuIleHisVa 95
 QY 671 CCAGCAATGGGAGGAGGACGACGATACAAAGAACTGAGGATCGGGAAGATGAT 730
 Db 95 LGLnLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuI 115
 QY 731 CGTG 734
 |:::

Db 115 eLeu 116
 RESULT 14
 US-08-470-298B-7
 ; Sequence 7, Application US/08470298B
 ; Patent No. 5844081
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER
 ; APPLICANT: YU, GUO-LIANG
 ; APPLICANT: ROSEN, CRAIG A.
 ; TITLE OF INVENTION: CYTOSTATIN I
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,298B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ALLAN A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF175D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8512
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: MDGI (FIGURE 2)
 ; US-08-470-298B-7
 Alignment Scores:
 Pred. No.: 1.17e-10 Length: 131
 Score: 163.50 Matches: 46
 Percent Similarity: 33.17% Conservative: 21
 Best Local Similarity: 22.77% Mismatches: 25
 Query Match: 7.30% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x US-08-470-298B-7 (1-131)
 QY 131 GGAGTAGGACTGGCTTATAGGAAGATGGCTGCATGCCAAGCCAGACTGTATCATTACG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
 QY 191 TGTGATGGAACAACATACGCTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
 QY 251 TGTAACTGGGAGAGTGTATGTAACACGACAGCTGTGGCAGAAACACTGAGTCA 310
 Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACA 370
 Db 83 ----- 83

QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAACTACTTTTATGAGTTGACTTTTTCATA 430
Db 83 -----
QY 431 AATTAGTAAAGTCCCAAGGACTAAGAAATGAAGACATCTTTATGAGTTTCTAGATCGAAAA 490
Db 83 -----
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 -----
QY 551 CGAAGACTTGTGAGTGGTGGTGGCTGCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 83 -----
QY 611 TAACTACCTGTATTTTTCAGACAGGTCTGCACCTTCCAAAGCGGTGCCCTGCTCCAGCA 670
Db 84 -----
QY 671 CGACCAATGGGACGGAAGAGACGACGATGATGATGATGATGATGATGATGATGATGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeuI 115
QY - 731 CGTG 734
Db 115 eLeu 116

RESULT 15
US-08-820-825-11
; Sequence 11, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-11

Alignment Scores: 1.18e-10 Length: 133
Pred. No.:

Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 2 Gaps: 1
US-09-788-074-2 (1-1279) x US-08-820-825-11 (1-133)
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGGCAACAACATCACGGTCAAAACGAGACGACGACTGAAGACGACTGTGTTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAAACGACGACTGATGGCAGAAAACTAGAGTCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATATGCATTAACAAT 370
Db 83 -----
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAACTACTTTTATGAGTTGACTTTTTCATA 430
Db 83 -----
QY 431 AATTAGTAAAGTCCCAAGGACTAAGAAATGAAGACATCTTTATGAGTTTCTAGATCGAAAA 490
Db 83 -----
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 -----
QY 551 CGAAGACTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 610
Db 83 -----
QY 611 TAACTACCTGTATTTTTCAGACGAGGTCTGCACCTTCCAAAGCGGTGCCCTGCTCCAGCA 670
Db 84 -----
QY 671 CCAGCAATGGGACGGAAGAGAGACGACGATGATGATGATGATGATGATGATGATGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeuI 115
QY 731 CGTG 734
Db 115 eLeu 116
Search completed: November 25, 2002, 10:34:01
Job time : 20.5 secs

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GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model
Run on: November 25, 2002, 10:24:12 ; Search time 61 Seconds
(without alignments)
5587.788 Million cell updates/sec

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Perfect score: 2239
Sequence: 1 aatgggagcaatcgtacg.....tctatgagaaggtgcaatga 1279

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=dlsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US09788074 -ECGN.1.1.43 @runat_25112002_093513.15657 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	406.5	18.2	135	22	AAU08673
2	364.5	16.3	146	23	ABG60208
3	350.5	15.7	135	15	AAR55866
4	350.5	15.7	135	22	ABG08674
5	345.5	15.4	158	22	ABG27577
6	336.5	15.0	135	23	ABG61772
7	300.5	13.4	134	22	AAU08666
8	300.5	13.4	163	22	AAU08665
9	224	10.0	79	22	ABG13616
10	219	9.8	522	22	ABG13615
11	195	8.7	181	22	ABG13617
12	189.5	8.5	136	19	AAW40227
13	182	8.1	172	22	AAU10059
14	178	7.9	136	19	AAW40228
15	174.5	7.8	132	21	AAI90320
16	174.5	7.8	132	23	ABB08076
17	174	7.8	132	21	AAI90319
18	171.5	7.7	133	22	AAG66578
19	169.5	7.6	134	18	AAW31534
20	165.5	7.4	131	12	AAR13559
21	164.5	7.3	117	21	AAG03847
22	163.5	7.3	133	22	AAG66576
23	158.5	7.1	133	22	AAG66577
24	151.5	6.8	132	18	AAW22408
25	151.5	6.8	132	19	AAW80949
26	151.5	6.8	132	19	AAW81106
27	151.5	6.8	132	20	AAW82403
28	142.5	6.4	132	21	AAG03957
29	140	6.3	131	22	AAG66580
30	139.5	6.2	132	16	AAR75423
31	136	6.1	88	21	ABW58740
32	135	6.0	433	22	ABG27578
33	128	5.7	482	22	ABG18150
34	128	5.7	924	22	ABG13826
35	128	5.7	969	22	ABG24481
36	124	5.5	130	22	ABG62690
37	120	5.4	137	14	AAR42212
38	120	5.4	160	21	AAB43403
39	119	5.3	492	22	ABG28095
40	118	5.3	138	14	AAR42211
41	118	5.3	138	22	AAW76852
42	118	5.3	138	23	AAU85507
43	118	5.3	149	21	AAW85158
44	113	5.0	156	22	AAU02202
45	111.5	5.0	117	22	AAU30142

ALIGNMENTS

RESULT 1
AAU08673
ID AAU08673 standard; Protein; 135 AA.
XX
AC AAU08673;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse keratinocyte fatty acid binding protein, Mall.
XX
KW Mouse; Mal 1; keratinocyte fatty acid binding protein; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX
OS Mus musculus.
XX
PN WO200160384-A1.
XX
PD 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US05019.
XX 17-FEB-2000; 2000US-0183106.
XX (HARD) HARVARD COLLEGE.
XX Hotamisligil GS;
XX WPI; 2001-570550/64.
XX N-PSDB; AAS13246.
XX Reducing the level of circulating free fatty acids in a mammal, useful
XX for treating or preventing obesity, diabetes, dyslipidaemia or
XX atherosclerosis, by administering a keratinocyte lipid binding protein
XX inhibitor
XX
XX Disclosure; Page 2; 27pp; English.
XX
XX The invention relates to reducing the level of circulating free fatty
XX acids in a mammal comprising administering to a mammal a compound that
XX inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
XX fatty acid binding protein) or Mall activity. The method is useful for
XX reducing the level of circulating free fatty acids in a mammal,
XX particularly in a mammal that is suffering from or at risk of developing
XX obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
XX useful for diagnosing these diseases. The present sequence is Mouse
XX Mal 1.
XX
XX Sequence 135 AA;
SQ
Alignment Scores:
Pred. No.: 2,36e-37 Length: 135
Score: 406.50 Matches: 93
Percent Similarity: 45.02% Conservative: 2
Best Local Similarity: 44.08% Mismatches: 6
Query Match: 18.16% Indels: 110
DB: 22 Gaps: 1
US-09-788-074-2 (1-1279) x AAU08673 (1-135)
QY 131 GGAGTAGGACTGCTTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTAGC 190
Db 27 GlyValGlyLeuAlaLeuArgLysMetAlaAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACAACATCACGCTCAAACCCGAGAGACAGTGAAGACGACTGTGTCTCT 250
Db 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrThrValPheSer 66
QY 251 TGTACCTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTCAGGTCCAGC 310
Db 67 CysAsnLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
QY 311 TACAACATACTGTGAAGCCAGACAGACTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 85 ----- 85
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 85 ----- 85
QY 431 AATTAATAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 85 ----- 85
QY 491 GCACATAGTTGTATTGTGACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 85 ----- 85
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 85 ----- 85

QY 611 TAACTACCTGTATTTTTCAGACAGGCTGTGCACAGCTTCCAAAGAGGGTCCCTGTCCAGCA 670
Db 86 -----ValCysThrPheGlnAspGlyAlaLeuValGlnHi 97
QY 671 CCAGCAATGGAGCGGAGAGGAGACGACGATACAAAGAAAACTCAAGGATGGGAAGATGAT 730
Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetIi 117
QY 731 CGTGTGTGACATCAAAAGCACTGGCACCATGC 761
Db 117 eValGluCysValMetAsnAlaThrCys 127
RESULT 2
ABG60208
ID ABG60208 standard; Protein; 146 AA.
XX
AC ABG60208;
XX
DT 30-JUL-2002 (first entry)
XX Human DITHP polypeptide #266.
XX
KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW thymus.
XX
OS Homo sapiens.
XX
PN WO200220754-A2.
XX
PD 14-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27127.
XX
PR 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230583P.
PR 06-SEP-2000; 2000US-230505P.
PR 06-SEP-2000; 2000US-230514P.
PR 06-SEP-2000; 2000US-230515P.
PR 06-SEP-2000; 2000US-230517P.
PR 06-SEP-2000; 2000US-230518P.
PR 06-SEP-2000; 2000US-230519P.
PR 06-SEP-2000; 2000US-230595P.
PR 06-SEP-2000; 2000US-230597P.
PR 06-SEP-2000; 2000US-230598P.
PR 06-SEP-2000; 2000US-230599P.
PR 06-SEP-2000; 2000US-230610P.
PR 06-SEP-2000; 2000US-230865P.
PR 06-SEP-2000; 2000US-230988P.
PR 07-SEP-2000; 2000US-230951P.
PR 07-SEP-2000; 2000US-231163P.
PR 07-SEP-2000; 2000US-231167P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
DR N-PSDB; ABK71797.
XX

PT An isolated polynucleotide useful in diagnostics and therapeutics -
 XX
 PS Claim 29; page 679; 686pp; English.
 XX
 CC The invention relates to human diagnostic and therapeutic (dithp)
 CC polynucleotides and their associated polypeptides (DITHP polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
 CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
 CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
 XX
 SX Sequence 146 AA;

Alignment Scores:
 Pred. No.: 1-55e-32 Length: 146
 Score: 364.50 Matches: 84
 Percent Similarity: 42.86% Conservative: 6
 Best Local Similarity: 40.00% Mismatches: 10
 Query Match: 16.28% Indels: 110
 DB: 23 Gaps: 1

US-09-788-074-2 (1-1279) x ABG60208 (1-146)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTTAGG 190
 Db 32 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 51
 QY 191 TGTGATGGCAACATACAGCTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 52 LeuAspGlyAsnLeuThrValLysThrGluSerThrValLysThrValPheSer 71
 QY 251 TCTAACCTGGGAGAGAAAGTTTCATGAAGACAGCTGATGGCAGAAAACTGAGTCCAGC 310
 Db 72 CysThrLeuGlyGluLysPheAspGluThrAlaAspGlyArgLysThrGluThr 90
 QY 311 TACAACATACCTGTGAAGCAGACAGACTTCTAGATTTCACAGATTAAATTCATTAAACAAT 370
 Db 90 ----- 90
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAATAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 90 ----- 90
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCAAAA 490
 Db 90 ----- 90
 QY 491 GCACATAGTTGTTATTGTGAACAAATACGTATATCATGGGTGGGAGTTTCAGAGAGGAAAGG 550
 Db 90 ----- 90
 QY 551 CGAAGACTGTTGGAGTGGTGTGGGTCTCGGGGTTCTTCACTTTGGGAAGATGATGAAC 610
 Db 90 ----- 90
 QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAAGAGCGTGCCTGCTCCAGCA 670
 Db 91 -----ValCysThrPheThrAspGlyAlaLeuValGlnHr 102
 QY 671 CCAGCAATGGGAGGAGGAGCAGCAGTAAACAGAAACTGAAGGATGGGAAGATGAT 730
 Db 102 scLysTrpGluGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetVa 122

QY 731 CGTGGTGGACATCAAGACGACTGGCACCA 758
 Db 122 iValGluCysValMetAsnCysPro 131
 RESULT 3
 AAR55866
 ID AAR55866 standard; Protein; 135 AA.
 XX
 AC AAR55866;
 DT 07-DEC-1994 (first entry)
 XX
 DE Melanogenic inhibitor.
 XX
 KW Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;
 KW depigmentation; melanoma.
 XX
 OS Homo sapiens.
 XX
 PN WO9412534-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 16-NOV-1993; 93WO-US11139.
 XX
 PR 24-NOV-1992; 92US-0980513.
 PR 01-SEP-1993; 93US-0115172.
 XX
 PA (UYCI-) UNIV CINCINNATI.
 XX
 PI Farooqui JZ, Nordlund JJ;
 XX
 DR WPI; 1994-200198/24.
 DR N-PSDB; AAQ66842.
 XX
 PT Prodn. of a protein for inhibiting melanogenesis - useful for
 PT treating hyper-pigmentary diseases, destroying melanoma cells and
 PT for lightening unwanted body hair
 XX
 PS Disclosure; Page 5; 40pp; English.
 XX
 CC PCR primers given in AAQ66843-44 were used to amplify RNA from
 CC human skin previously grafted onto nude mice, thereby providing
 CC DNA (AAQ66842) encoding melanogenic inhibitor protein (AAR55866).
 XX
 SX Sequence 135 AA;
 Alignment Scores:
 Pred. No.: 6e-31 Length: 135
 Score: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 15 Gaps: 1
 US-09-788-074-2 (1-1279) x AAR55866 (1-135)
 QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTTAGG 190
 Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCAACGCTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TCTAACCTGGGAGAGAAAGTTTCATGAAGACAGACTGATGGCAGAAAACTGAGTCCAGC 310
 Db 67 CysThrLeuGlyGluLysPheGluThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACCTGTGAAGCAGCAGAGCTTCTAGATTTCACAGATTAAATTCATTAAACAAT 370
 Db 84 ----- 84

QY 371 GTCTGTACTTACTGCCAAGGCTGACTGATAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 -----
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
 Db 84 -----
 QY 491 GCACATAGTTGATTGTGAACAAATCAGTATCATGGGTGGAGTTCACAGAGGGAAGG 550
 Db 84 -----
 QY 551 CGAAGACTTGTGGAGTGTGGTCTGGTGGGTTCCTTCACTTGGGAAGATGATGAAC 610
 Db 84 -----
 QY 611 TAACTACCTGTATTTTGCACAGGCTCTGCACCTTCCAAAGCGTGCCTGGTCCAGCA 670
 Db 85 -----
 QY 671 CCAGCAATGGGAGGAGGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGAGCATCAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127

RESULT 4
 AAU08674
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 DT 18-DEC-2001 (first entry)
 DE Human keratinocyte fatty acid binding protein, Mall.
 KW Human; Mall 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antisense therapy.
 OS Homo sapiens.
 PN WO200160384-A1.
 PD 23-AUG-2001.
 PF 16-FEB-2001; 2001WO-US05019.
 PR 17-FEB-2000; 2000US-0183106.
 PA (HARD) HARVARD COLLEGE.
 PI Hotamisligil GS;
 DR WPI; 2001-570550/64.
 DR N-PSDB; AAS13247.
 XX
 PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor -
 XX
 PS Disclosure; Page 2; 27pp; English.
 XX
 CC The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
 CC fatty acid binding protein) or Mall activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also

CC useful for diagnosing these diseases. The present sequence is Human
 CC Mall 1.
 XX
 SQ Sequence 135 AA;
 Alignment Scores:
 Score: 6e-31 Length: 135
 Pred. No.: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 22 Gaps: 1
 US-09-788-074-2 (1-1279) x AAU08674 (1-135)
 QY 131 GGAGTAGGACTGGCTCTTAGGAGAGATGGTCCATCGCCCAAGCCAGACTGTATCATTCAG 190
 Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACAATCATCACGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrGlnPheSer 66
 QY 251 TGTAACTGGGAGAGAAAGTTTGTATGAACACAGCAGCTGTATGGCAAAAACCTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGlyLysPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACTGTGAAGCGACAGAACCTTCTAGATTACAGATTAATTCATTACAAT 370
 Db 84 -----
 QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 -----
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
 Db 84 -----
 QY 491 GCACATAGTTGATTGTGAACAAATCAGTATCATGGGTGGAGTTCAGAGAGGGAAGG 550
 Db 84 -----
 QY 551 CGAAGACTTGTGGAGTGTGGTCTGGTGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 84 -----
 QY 611 TAACTACCTGTATTTTGCACAGGCTCTGCACCTTCCAAAGCGTGCCTGGTCCAGCA 670
 Db 85 -----
 QY 671 CCAGCAATGGGAGGAGGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGAGCATCAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 5
 ABG27577
 ID ABG27577 standard; Protein; 158 AA.
 XX
 AC ABG27577;
 XX
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #27568.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX PF 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX N-PSDB; AAS91764.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 20; SEQ ID No 57936; 103pp; English.

*The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from wipo at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 158 AA;

Alignment Scores:
Pred. No.: 2,398-30 Length: 158
Score: 345.50 Matches: 77
Percent Similarity: 41.23% Conservative: 10
Best Local Similarity: 36.49% Mismatches: 14
Query Match: 15.43% Indels: 110
DB: 22 Gaps: 1

US-09-788-074-2 (1-1279) x ABG27577 (1-158)

QY 131 GGAGTAGGACTGGCTTTAGGAAGATGGCTGCCATGGCCAGCAGCTGTATCATTCAG 190
Db 50 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetProLysPronaspCysIleIleThr 69
QY 191 TGTGATGGCAACATCATCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 70 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 89
QY 251 TGTACCTGGGAGAGAAAGTTTCAAGACGACAGCTGTGGCAGAGAAATCAGGTACGC 310
Db 90 CysThrLeuGlyGlyLysPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 107
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATGTCATTACAT 370
Db 107 -----

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 107 -----
QY 431 AATTAGTAAAGTCCCGAGCTAAGAAATGAAGACATCTTATCAGTTTCTAGATCGAAAA 490
Db 107 -----
QY 491 GCACATAGTTGTTATTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAG 550
Db 107 -----
QY 551 CGAAGACTGTTGGAGCTGCTGGGTCTCGGGGTTTCCTTACTTTGGAGATGATGAAC 610
Db 107 -----
QY 611 TAACTACCTGTATTTTTCAGACGCTGTCACCTTCCAAAGAGCGTCCCTGGTCCAGCA 670
Db 108 -----ThrValCysAsnPheThrArgLysLeuLysAspGlyLysLeuValGlnHl 120
QY 671 CCAGCAATGGGAGGAGGAGACGACGATACAAAGAACTGAAGATGGGAGATGAT 730
Db 120 SGLnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 140
QY 731 CGTGTGACGATCAAGACGACTGGCACCACATGC 761
Db 140 lValGluCysValMetAsnValThrCys 150
RESULT 6
ABG61772
ID ABG61772 standard; Protein; 135 AA.
XX AC ABG61772;
XX DT 14-AUG-2002 (first entry)
XX DE Novel fatty acid-binding protein-like protein.
XX KW Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;
KW behavioral disorder; valve disease; endocrine disorder; heart disorder;
KW blood disorder; anxiety disorder; brain disorder; inflammatory disorder;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
KW gene therapy; transgenic animal; human.
XX OS Homo sapiens.
XX PN WO200229058-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US31248.
XX PR 05-OCT-2000; 2000US-238323P.
PR 05-OCT-2000; 2000US-238325P.
PR 06-OCT-2000; 2000US-238372P.
PR 06-OCT-2000; 2000US-238373P.
PR 06-OCT-2000; 2000US-238379P.
PR 06-OCT-2000; 2000US-238382P.
PR 06-OCT-2000; 2000US-238383P.
PR 06-OCT-2000; 2000US-238384P.
PR 06-OCT-2000; 2000US-238397P.
PR 06-OCT-2000; 2000US-238400P.
PR 06-OCT-2000; 2000US-238401P.
PR 06-OCT-2000; 2000US-238402P.
PR 14-MAR-2001; 2001US-275892P.
PR 08-JUN-2001; 2001US-296860P.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Taupler RJ, Burgess CE, Zerhusen BD, Mezes PS;
PI

CC pathology associated with NOVX polypeptide in humans and for treating a
 CC syndrome associated with human disease e.g. disorders characterised by
 CC altered cell motility, proliferation and migration e.g. cancer,
 CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
 CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
 CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
 CC asthma, hypertension and seizure (NOV4), enamel defects, such as
 CC amelogenesis imperfecta and disorders involving enamel defects,
 CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
 CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
 CC encephalitis occurring during testicular cancer, diabetes, reproductive
 CC health, metabolic and endocrine disorders, gastrointestinal disorders,
 CC immune disorders and autoimmune diseases, respiratory disorders, bone
 CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
 CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
 CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
 CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
 CC binds to it and a cell expressing NOVX polypeptide is useful for
 CC identifying a therapeutic agent for use in treatment of a NOVX related
 CC pathology. The antibodies and a polypeptide having 95% sequence identity
 CC to NOVX polypeptide are useful for treating a pathological state in a
 CC mammal. The present sequence represents NOV10, a possible epidermal
 CC fatty acid-binding protein family member.
 XX
 SQ •Sequence 134 AA;

Alignment Scores:
 Pred. No.: 3,12e-25 Length: 134
 Score: 300.50 Matches: 68
 Percent Similarity: 39.80% Conservative: 12
 Best Local Similarity: 33.83% Mismatches: 11
 Query Match: 13.42% Indels: 110
 DB: 22 Gaps: 1

US-09-788-074-2 (1-1279) x AAU08666 (1-134)

QY 131 GGAGTAGGACTGGCTCTTAGGAGATGGCTGCCATGGCCAGCCAGCTGTATCATTCAG 190
 Db 27 GllYValGlyLeuSerLeuArgAsnMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTCGGAGAGAGTTGTGTAACACACAGCTGATGGCAGAAAACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGlyLysPheGluGlyThrThrAlaValGlyArgLysThr-Gln----- 84
 QY 311 TACAACACTACTGTGAAGCCAGACAGAACTTCTAGATTTCACAGATTAAATTCACAAAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAACAACTTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 ----- 84
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATCAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTGTTGGAGCTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 84 ----- 84
 QY 611 TAACTACCTGTATTTTTCAGACAGCTGTGCACCTTCCAAGAGCGGTGCCCTGTCAGCA 670
 Db 85 -----ThrValCysSerPheThrAspGlyAlaLeuValProHl 97
 QY 671 CCAGCAATGGGACGGGAGGAGACGACGATACAGAAAACTGAAGGATGGGAAGATGAT 730

bb 97 sGlnGluTrpAspGlyLysGluAsnThrIleThrArgLysLeuLysAspAlaSerValva 117
 QY 731 C 731
 Db 117 I 117
 RESULT 8
 AAU08665
 ID AAU08665 standard; Protein: 163 AA.
 XX
 AC AAU08665;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human NOV9 protein.
 XX
 KW Human; NOV9; cytostatic; nootropic; neuroprotective; vulnary;
 KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
 KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
 KW antiatherosclerotic; dermatological; cancer; neurological disorder;
 KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
 KW immune disorder; autoimmune disease; respiratory disorder;
 KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
 KW cell growth regulation disorder; lesional psoriatic skin;
 KW atherosclerosis; abdominal aortic aneurysm.
 XX
 OS Homo sapiens.
 XX
 PN WO200168851-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 12-MAR-2001; 2001WO-US07735.
 XX
 PR 10-MAR-2000; 2000US-0188277.
 PR 10-MAR-2000; 2000US-0188316.
 PR 14-MAR-2000; 2000US-0189139.
 PR 14-MAR-2000; 2000US-0189140.
 PR 17-MAR-2000; 2000US-0190231.
 PR 17-MAR-2000; 2000US-0190401.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;
 PI Majumder K, Li L;
 XX
 WPI: 2001-570869/64.
 DR N-PSDB; AAS13343.
 XX
 PT Novel polypeptides and nucleic acids homologous to members of collagen,
 PT potassium channel, tuftelin family of proteins for diagnosing, treating
 PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
 XX
 PS Claim 9; Page 34; 128pp; English.
 XX
 CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and
 CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
 CC and anti-NOVX antibodies are useful for treating or preventing a
 CC pathology associated with NOVX polypeptide in humans and for treating a
 CC syndrome associated with human disease e.g. disorders characterised by
 CC altered cell motility, proliferation and migration e.g. cancer,
 CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
 CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
 CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
 CC asthma, hypertension and seizure (NOV4), enamel defects, such as
 CC amelogenesis imperfecta and disorders involving enamel defects,
 CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
 CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
 CC encephalitis occurring during testicular cancer, diabetes, reproductive
 CC health, metabolic and endocrine disorders, gastrointestinal disorders,
 CC immune disorders and autoimmune diseases, respiratory disorders, bone
 CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
 CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
 CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
 CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
 CC binds to it and a cell expressing NOVX polypeptide is useful for
 CC identifying a therapeutic agent for use in treatment of a NOVX related
 CC pathology. The antibodies and a polypeptide having 95% sequence identity
 CC to NOVX polypeptide are useful for treating a pathological state in a
 CC mammal. The present sequence represents NOV10, a possible epidermal
 CC fatty acid-binding protein family member.

CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
 CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
 CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
 CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
 CC binds to it and a cell expressing NOVX polypeptide is useful for
 CC identifying a therapeutic agent for use in treatment of a NOVX related
 CC pathology. The antibodies and a polypeptide having 95% sequence identity
 CC to NOVX polypeptide are useful for treating a pathological state in a
 CC mammal. The present sequence represents NOV9, a possible epidermal
 CC fatty acid-binding protein family member.
 XX
 SQ Sequence 163 AA;

Alignment Scores: 3.4e-25 Length: 163
 Pred. No.: 300.50 Matches: 68
 Score: 39.80% Conservative: 12
 Percent Similarity: 33.83% Mismatches: 11
 Best Local Similarity: 13.42% Indels: 110
 Query Match: 22 Gaps: 1
 DB:

US-09-788-074-2 (1-1279) x AAU08665 (1-163)

QY 131 GGAGTAGGACTGCTCTTAGGAGATGGTGCATCGGCAAGCCAGCACTGTATCATACG 190
 Db 56 GlyValGlyLeuSerLeuArgAsnMetGlyAlaMetAlaLysProAspCysIleIleThr 75
 QY 191 TGTGATGGCAACATCATCGGTCFAAACCGGAGACGACAGTGAAGACGTGGTGTCTCT 250
 Db 76 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 95
 QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAAAAACACTGAGGTCAGC 310
 Db 96 CysThrLeuGlyLysPheGluGlyThrThrAlaValGlyArgLysThr-Gln----- 113
 QY 311 TACAACATCTGTGAGCCACAGAACCTCTAGATTACAGATTAAATTGCATTACAAAT 370
 Db 113 ----- 113
 QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACCTACTTTATGGAGTTGACTTTTGATA 430
 Db 113 ----- 113
 QY 431 AATTAGTAAAGTCCAGGACTAAGAATGAACATCTTATGAGTTCTAGATCGAAAA 490
 Db 113 ----- 113
 QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGATTCAGAGAGGAAAGG 550
 Db 113 ----- 113
 QY 551 CGAAGACTTGTGGAGTGGTGGTCCCTGGGGTTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 113 ----- 113
 QY 611 TAACCTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
 Db 114 -----ThrValCysSerPheThrAspGlyAlaLeuValProIle 126
 QY 671 CCAGCAATGGCGGGAAGGAGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
 Db 126 sGlnGluTrpAspGlyLysGluAsnThrIleThrArgLysLeuLysAspAlaSerValVa 146
 QY 731 C 731
 Db 146 i 146

RESULT 9
 ID ABG13616
 XX ABG13616 standard; Protein; 79 AA.
 AC
 XX ABG13616;

DT 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #13607.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS77803.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 XX Claim 20; SEQ ID No 43975; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymetase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABC00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 79 AA;

Alignment Scores:
 Pred. No.: 1.4e-16 Length: 79
 Score: 224.00 Matches: 43
 Percent Similarity: 76.12% Conservative: 8
 Best Local Similarity: 64.18% Mismatches: 16
 Query Match: 10.00% Indels: 0
 DB: 22 Gaps: 0

US-09-788-074-2 (1-1279) x ABG13616 (1-79)

QY 615 TACCTGTATTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCACG 674
 Db 8 PheThrLeuPheLeuGlnThrValCysAsnPheThrAspGlyAlaLeuValGlnHisGln 27
 QY 675 CAATGGGACGGAGGAGACGACGATACAAAGAAACTGAAGGATGGGAGATGATCGG 734
 Db 28 GluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuValVal 47

QY 735 GTGACATCAAGCACTGCACCATCTGGGATTTGGGCTGCAGCCACAGTTGTTCATAC 794
|||||:||||| ||| ||| ||||| |||||
Db 48 ValSerValLysLeuLeuLeuLeuLeuLeuValCysIleHisSerHisAsn 67
795 CACTTCGGGTCTATTGTTCTT 815
|||||:|||||
Db 68 CysSerIleSerLeuIleIle 74

RESULT 10
ID ABG13615 standard; Protein; 522 AA.
XX AC ABG13615;
XX 18-FEB-2002 (first entry)
DT Novel human diagnostic protein #13606.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR N-PSDB; AAS77802.

New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

Claim 20; SEQ ID NO 43974; 103pp; English.

The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 522 AA;
Alignment Scores: 1.17e-15 Length: 522
Pred. No.:

Score: 219.00 Matches: 62
Percent Similarity: 42.71% Conservative: 20
Best Local Similarity: 32.29% Mismatches: 48
Query Match: 9.78% Indels: 62
DB: 22 Gaps: 7

US-09-788-074-2 (1-1279) x ABG13615 (1-522)

QY 164 ATGGCCAGCCAGACTGTATCATTTACGTGTGTCGCAACACATCAGGTCAAAACCGAG 223
|||||:||||| ||| ||| ||||| |||||
Db 1 MetAlaLysProAspCysIleIleThrCysAspSerLysAsnLeuThrIleLysThrGlu 20

QY 224 AGCAGACTGAACAGCACTCTGTTCTTCTTAACCTGGGAGAGAACTTTCATGAACGACA 283
|||||:||||| ||| ||| ||||| |||||
Db 21 SerThrLeuLysThrGlnPheSerGlyThrLeuGlyGluPheGluAsnThr 40

QY 284 GCTGATGGCAGAAAAAAGTCACTGAGTCAACATACATCTGAAGGCACAGAAGCTTCTAG 343
|||||:||||| ||| ||| ||||| |||||
Db 41 AlaAspGlyArgArgThrGln----- 47

QY 344 ATTTACAGATTAAATTCATTAAACAATGCTCTACTTACTGCCAAGGGCTGACTGAAAAA 403
|||||:||||| ||| ||| ||||| |||||
Db 48 -----ThrValCysAsnPheThrAspGly----- 55

QY 404 ACTACTTTATGAGTTGACTTTTGTATAAATTAGTAAAGTCCAGGACTAAGAAATGAAG 463
|||||:||||| ||| ||| ||||| |||||
Db 56 -----ArgSerGluAspThrGluMetAsn 63

QY 464 ACATCTTATGAGTTCTA---GATCGAAAAGCACATAGTTGTATTGTGAACAAATCACT 520
|||||:||||| ||| ||| ||||| |||||
Db 64 ValLeuIleSerAlaLeuGlnGluHisSerSerArgAsnProValLysAsnLeuLeuPhe 83

QY 521 ATGATGGGTGGAGTTTCAGAGAGGGAAGCGGAAGACTTTGTTGGAGTGTGTGGTCTCG 580
|||||:||||| ||| ||| ||||| |||||
Db 84 ArgLeuGlyPheArgAlaSerLeuGln----- 92

QY 581 GGGGTTCTTCACTTTGGGAAGATGATGAATACTACCTGTATTTTTCAGACAGCGTCTG 640
|||||:||||| ||| ||| ||||| |||||
Db 93 -----ProThrValAlaSer-----ProLeuSerAlaGlyHisGlyGln 105

QY 641 CACCTTCCAAAGACGGTGCCTGTCAGCAGCAGCAATGGGACGGGAGGAGACGAT 700
|||||:||||| ||| ||| ||||| |||||
Db 106 HisSerPro---PheSerProGlyAlaAlaProAlaAlaGlyThrGlu----- 120

QY 701 AACAAAGAAACTGAAGGATGGGAAGATGATCGTGT 736
|||||:||||| ||| ||| ||||| |||||
Db 121 ---ProLysGlyGluProLysGluSerGlyArgGly 131

RESULT 11
ABG13617
ID ABG13617 standard; Protein; 181 AA.
XX AC ABG13617;
XX 18-FEB-2002 (first entry)
DT Novel human diagnostic protein #13608.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS77804.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 43976; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 181 AA;

Alignment Scores:

Pred. No.: 4, 13e-13 Length: 181
 Score: 195.00 Matches: 64
 Percent Similarity: 37.50% Conservativity: 14
 Best Local Similarity: 30.77% Mismatches: 16
 Query Match: 8.71% Indels: 114
 DB: 22 Gaps: 7

US-09-788-074-2 (1-1279) x ABG13617 (1-181)

QY 131 GGAGTAGGACTGGCTTAGGAAGATGGCTGCCATGGCGCAAGCCAGAC---TGATATCAT 187
 DB 66 GlyValThrIleAlaLeuArgLysMetGlyArgAsnAlaGlnAlaGlnIleCysIlelle 85
 QY 188 ACGTGTGTATGGCAACACATCAG---GTCAAACCGCAGACAGTGAAGAGCTGTG 244
 DB 86 ThrSerAspGly***AsnProSerProLeuLysThrGluSerThrLeuLysThrThrGln 105
 QY 245 TTCTCTTGTAACTG---GGAGAGAAGTTTGTAAACACACAGCTGATGGCAGAAACT 301
 DB 106 PheSerCysThrLeuTrpGlyGlyLysPheGluGluThrThrAlaAspGlyGlnLysLys 125
 QY 302 GAGGTGAGTACACATACACTGTGAAGCGGACAGAGAGCTTCTAGATTACAGATTAAATTC 361
 DB 126 -----LeuThrAsnCys 129
 QY 362 ATTAACAATGTCTGTACTTACTGCCAAGGCTGACTGAAAAAATCTATTATGAGATTGA 421
 DB 130 -LeuSer----- 131
 QY 422 CTTTGTATAAATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTA 481
 DB 131 ----- 131
 QY 482 GATCGAAAAGCACATAGTTGTATTCTGAACAAATACAGTATGATGGGTGAGTTTCAGAG 541

Db 131 ----- 131
 QY 542 AGGGAAGCGAAGACTTGTGGAGTGGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAG 601
 Db 131 ----- 131
 QY 602 ATGATGAACAACTACCTGCTATTATTTTGCAGACGGTCTGCACCTTCCAAAGACGGTCCCT 661
 Db 132 -----ThrPheProAspGlyAla 138
 QY 662 GGTCCAGCACCAATGGACGGG---AAGGAGACGACGATACAAAGAAA---CTGAA 715
 Db 138 uValGlnHisGlnGluTrpAspGlyGluArgLysSerThrIleThrLysAsn***Ly 158
 QY 716 GGATGGGAAGATGATCGTG 735
 Db 158 sAspGlyGluIle-SerTrp 164
 RESULT 12
 AAW40227
 ID AAW40227 standard; Protein; 136 AA.
 AC AAW40227;
 DT 26-JUN-1998 (first entry)
 DE Human myelin P2 protein.
 KW Human; myelin; P2 protein; treatment; inflammatory polyneuritis;
 KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
 KW gammopathy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 49 /note= "encoded by AAT"
 FT
 PN WO9803647-A2.
 XX 29-JAN-1998.
 PD 18-JUL-1997; 97WO-DE01535.
 PF 18-JUL-1996; 96DE-1029095.
 PR (GOLD/) GOLD R.
 PA (WEIS/) WEISHAAPT A.
 PI Gold R, Weishaupt A;
 DR WPI; 1998-120772/11.
 DR N-PSDB; AAV10405.
 XX
 PT Recombinant myelin proteins for treating T-cell mediated disease of
 PT peripheral nervous system - by high dose antigen therapy, causing
 PT apoptosis in T cells, for treating e.g. polyneuritis or
 PT Guillain-Barre syndrome
 XX
 PS Disclosure; Fig 4; 14pp; German.
 CC The present sequence is the human myelin P2 protein, which can
 CC be used to treat T-cell mediated diseases of the peripheral nervous
 CC system, especially chronic-inflammatory polyneuritis,
 CC Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
 CC of gammopathy.
 XX
 SQ Sequence 136 AA;
 Alignment Scores:
 Pred. No.: 1.56e-12 Length: 136
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservativity: 16

Best Local Similarity:	26.37%	Mismatches:	22
Query Match:	8.46%	Indels:	110
DB:	19	Gaps:	1
US-09-788-074-2 (1-1279) x AAU40227 (1-136)			
QY	131	GGAGTAGGACTGGCTCTTAGGAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTTACG	190
Db	25	GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer	44
QY	191	TGTGATGGCAACAATCATCGGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT	250
Db	45	LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer	64
QY	251	TGTAACTCGGAGAGAGTGTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTGACG	310
Db	65	PheLysLeuGlyGlnGluPheGluGluThrThrAlaAspAsnArgLysThr-LysSer--	83
QY	311	TACAACATCTGTGAAGCCACAGACCTTCTAGATTACAGATTAATTCGCATTAACAAT	370
Db	83	-----	83
QY	371	GTCTGTACTTACTGCCAAGGCTGACTGAAAAACTTCTTATGGAGTTGACTTTTGATA	430
Db	83	-----	83
QY	431	AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA	490
Db	83	-----	83
QY	491	GCACATAGTTGTATTTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAGG	550
Db	83	-----	83
QY	551	CGAAGACTGTTGGAGTGTGTGGTCTCTGCGGTTCTTCACTTTGGAAGATGATGAAC	610
Db	83	-----	83
QY	611	TAACTACCTGTATTTTTCAGACAGCTGTCACCTTCCAAAGCGGTGCTGTCAGCA	670
Db	84	-----IleValThrLeuGlnArgGlySerLeuAsnGlnVa	95
QY	671	CGAGCAATGGGAGGAGGAGACGACGATACACAGAAACTGAAGATGGGGAAGATGAT	730
Db	95	lGlnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa	115
QY	731	C 731	
Db	115	i 115	
RESULT	13		
ID	AAU10059		
AC	AAU10059 standard; Protein; 172 AA.		
XX			
AC	AAU10059;		
XX			
DT	14-FEB-2002 (first entry)		
DE			
XX	Fatty acid-binding family associated protein, NOV2.		
KW	NOV; cytostatic; psoriasis; neutropic; neuroprotectant;		
KW	cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;		
KW	haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;		
KW	differentiation; proliferation; haematopoiesis; wound healing;		
KW	angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;		
KW	haemophilia; allergy; Pendred syndrome; skeletal dysplasia;		
KW	ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;		
KW	fatty acid-binding protein; FAPP; chromosome 5.		
OS	Homo sapiens.		
XX			
PN	WO200170978-A2.		
XX			

PD	27-SEP-2001.		
XX			
PF	20-MAR-2001; 2001WO-US09093.		
XX			
PR	20-MAR-2000; 2000US-190768P.		
PR	20-MAR-2000; 2000US-190835P.		
PR	22-MAR-2000; 2000US-190972P.		
PR	22-MAR-2000; 2000US-191199P.		
PR	24-MAR-2000; 2000US-191947P.		
PR	28-MAR-2000; 2000US-192657P.		
PR	28-MAR-2000; 2000US-192664P.		
PR	28-MAR-2000; 2000US-192665P.		
PR	28-MAR-2000; 2000US-192864P.		
PR	29-MAR-2000; 2000US-192836P.		
XX			
PA	(CURA-) CURAGEN CORP.		
PI	Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;		
PI	Vernet CAM;		
XX			
DR	WPI; 2001-639127/73.		
DR	N-PSDB; AAS15722.		
XX			
PT	Polypeptides and nucleic acids related to chloride channel,		
PT	insulin-like growth factor family of proteins, useful for diagnosing		
PT	and treating cancer, cystic fibrosis, acute pancreatitis and		
PT	Alzheimer's disease -		
XX			
PS	Claim 1; Page 11; 151pp; English.		
XX			
CC	The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX		
CC	polypeptides are useful for treating pathology associated with NOVX		
CC	polypeptide, determining the presence of or predisposition to a disease		
CC	associated with altered levels of NOVX, identifying agents binding to		
CC	NOVX and treatment of disorders associated with altered expression of		
CC	members of chloride channel-associated proteins e.g. cystic fibrosis and		
CC	congenital myotonia. NOVX proteins are useful in treatment of disorders		
CC	including psoriasis, cancer, diabetes, metabolic disorders of pancreas,		
CC	e.g. acute pancreatitis, abnormal growth and accumulation of mast cells		
CC	in one or more organs (e.g. haemophilia, anaemia), Pendred syndrome,		
CC	skeletal dysplasias, disorders characterised by altered cell shape,		
CC	motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial		
CC	disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the		
CC	treatment of disorders of vascular smooth muscle cell differentiation,		
CC	(e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are		
CC	useful to screen for molecules which inhibit or enhance NOVX activity or		
CC	function and are useful as targets for the identifying small molecules,		
CC	that modulate or inhibit e.g. neurogenesis, proliferation, motility,		
CC	cell differentiation, haematopoiesis, wound healing and angiogenesis. NOV		
CC	sequences are also useful for: identifying a cell or tissue type in a		
CC	biological sample; amplifying DNA sequences from very small biological		
CC	samples e.g. hair or skin or body fluids and as primers and probes to		
CC	identify and/or clone NOVX homologues. NOVX proteins are useful		
CC	immunogens to generate antibodies to monitor protein levels and modulate		
CC	NOVX activity. Cells comprising the nucleic acids are useful for		
CC	producing transgenic animals, for studying the function and/or activity		
CC	of NOVX protein and identifying and/or evaluating modulators of NOVX		
CC	protein activity. This sequence is the NOV2 amino acid sequence (the gene		
CC	is located on chromosome 5) related to the fatty acid-binding protein		
CC	family proteins, one of 12 NOV polypeptides described in the method of		
CC	the invention.		
XX			
SQ	Sequence 172 AA;		
Alignment Scores:			
Pred. No.:	1,24e-11	Length:	172
Score:	182.00	Matches:	55
Percent Similarity:	32.51%	Conservative:	11
Best Local Similarity:	27.09%	Mismatches:	24
Query Match:	8.13%	Indels:	113
DB:	22	Gaps:	3
US-09-788-074-2 (1-1279) x AAU10059 (1-172)			

```
QY 131 GGAGTAGGACTGGCTCTT---AGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATATCATT 187
D 131 |||||
Db 65 GlyValGlyLeuAlaLeuCysGluLysGlyAlaMetAlaLysLysAspCysIleSer 84
QY 188 ACGTGTGATGGCAACAACATCACGGTCAAAACCGAGACAGACAGTGAAGACGACTGTGCTTC 247
D 188 |||||
Db 85 PhePheAspGlyLysAsnLeuThrIleLysMetGluSerThrLeuLysSerTyrSerPhe 104
QY 248 TCTTGTAACTGGGAGAGAGATTGTGAACACAGACAGCTGATGCGAGAAAACCTGAGTC 307
D 248 |||||
Db 105 LeuThrLeuArgGlyGlyLysPheLysGluThrThrGlyAspGlyArgLysThrGln-Th 124
QY 308 AGCTAACACATACTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATGCATTAAC 367
D 308 ;
Db 124 r----- 124
QY 368 AATGCTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACITTTG 427
D 368 ----- 124
QY 428 ATAAATAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGA 487
D 428 ----- 124
QY 488 AAAGCACATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAA 547
D 488 ----- 124
QY 548 AGCGAAGACTTGTGGAGTGGTGTGGTCTCTGGGGTTCCTTCACCTTGGGAAGATGATG 607
D 548 ----- 124
QY 608 AACTAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCA 667
D 608 |||||
Db 125 -----CysThrPheThrTyrGlyThrLeuValar 134
QY 668 GCACCGACCAATGGACGGGAAGGAGACGACGATACAAAGAAAACCTGAAGATGGGAAGAT 727
D 668 :|||
Db 134 gHisGlnLysTrpAsnGlyLysGluGlyLysIle---ArgLysLeuLysAspArgLysLe 153
QY 728 GATCGTG 734
D 728 :|||
Db 153 uValVal 155
RESULT 14
AAW40228
ID AAW40228 standard; Protein; 136 AA.
XX
AC AAW40228;
XX
DT 26-JUN-1998 (first entry)
XX
DE Bovine myelin P2 protein.
XX
KW Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy.
XX
OS Bos taurus.
XX
PN WO9803647-A2.
XX
PD 29-JAN-1998.
XX
PF 18-JUL-1997; 97WO-DE01535.
XX
PR 18-JUL-1996; 96DE-1029095.
XX
PA (GOLD/) GOLD R.
PA (WEIS/) WEISHAUP A.
PX Cold R, Weishaupt A;
PI
```

```
XX WPI; 1998-120772/11.
XX
XX Recombinant myelin proteins for treating T-cell mediated disease of
PT peripheral nervous system - by high dose antigen therapy, causing
PT apoptosis in T cells, for treating e.g. polyneuritis or
PT Guillain-Barre syndrome
XX
PS Disclosure; Fig 4; 14pp; German.
XX
XX The present sequence is the bovine myelin P2 protein, which can
CC be used to treat T-cell mediated diseases of the peripheral nervous
CC system, especially chronic-inflammatory polyneuritis,
CC Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
CC of gammopathy.
XX
SQ Sequence 136 AA;
Alignment Scores:
Pred. No.: 3.21e-11 Length: 136
Score: 178.00 Matches: 56
Percent Similarity: 33.19% Conservative: 19
Best Local Similarity: 24.78% Mismatches: 32
Query Match: 7.95% Indels: 119
DB: 19 Gaps: 4
US-09-788-074-2 (1-1279) x AAW40228 (1-136)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTACG 190
D 131 |||||
Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProValIleSer 44
QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGACAGACAGTGAAGACGACTGTGCTCT 250
D 191 |||||
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 64
QY 251 TGTAACTCTGGGAGAGAGTTTGTATGAACACAGACAGCTGATGCGAGAAAACCTGAGTCAGC 310
D 251 |||||
Db 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSerTh 84
QY 311 TACAACATCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATGCATTAACAAT 370
D 311 |||
Db 84 rValThrLeuAlaArg----- 89
QY 371 GTCTGTACTTACTGCCAAGGCGTGACTGAAAAAACTATTATGGAGTTGCTTTTCATA 430
D 371 ----- 89
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAGACATCTTATGAGTTTCTAGATCGAAAA 490
D 431 ----- 89
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
D 491 ----- 89
QY 551 CGAAGACTTGTGGAGTGGTGGTCTCGGGGGTTCCTTCACCTTTTGAAGATGATGAAC 610
D 551 ----- 89
QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
D 611 |||||
Db 90 -----GlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGACGGGAAGAGACAGACAGATACAAAGAAAACCTGAAGATGGGGAAGATGAT 730
D 671 |||||
Db 95 lGlnLysTrpAspGlyAsnGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 CGTG---GTGAGCATCAAAAGACACTGGCACCATCTCTGGGATTTGGCCCTGAGC-----CA 781
D 731 |||||
Db 115 lValGluCysLysMetLys-----AspValValCysThrArgIlefy 129
QY 782 CAGTTGTGCATAACCCAC 797
```

Db	129	rAspValHishHis 134	:	45	valAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer	64
RESULT 15						
AAAY90320	ID	AAAY90320 standard; Protein; 132 AA.		251	TGTAACCTGGGAGAGAAGTTTGATGAACGACAGACTGATGGCAGAAAAAACTGAGGTGCAGC	310
XX	XX			65	PheIleLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer--	83
AC	AAAY90320;			311	TACAACATACTGTGAAGCGACAGACCTTCTAGATTACAGATTAATAATTCATTAACAAT	370
XX	XX			83	----	83
DT	22-NOV-2000 (first entry)			371	GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA	430
DE	Human AFABP protein sequence.			83	----	83
XX	AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;			431	AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA	490
KW	lesion formation inhibition; macrophage; adipocyte; atherosclerosis;			83	----	83
serum cholesterol; therapy; human.				491	GCACATAGTTGTATTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG	550
XX	Homo sapiens.			83	----	83
OS	WO200047734-A1.			551	CGAAGACTTGTTGGAGTGGTGGGTCTCGGGGTTCCTTCACTTTGGAAGATGATGAAC	610
PN	17-AUG-2000.			83	----	83
XX	11-FEB-2000; 2000WO-US03560.			611	TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGCGGTCCCTGGTCCAGCA	670
PF	12-FEB-1999; 99US-0119880.			84	-----ThrIleThrLeuAspGlyValLeuValHisVa	95
PR	(HARD) HARVARD COLLEGE.			671	CCAGCAATGGGACGGGAAGGAGACGACGATAACACGAAAACTGAAGCATGGGAAGATGAT	730
PA	Lee M, Perrella MA, Hotamisligil GS;			95	lGlnLysTrpaspGlyLysSerThrThrIleLysArgLysArgGluaspLysLeuVa	115
XX	WPI; 2000-506094/45.			731	CGTG 734	
DR	N-PSDB; AAA37717.			115	lVal 116	
DR	Reducing expression of adipocyte fatty acid binding protein through					
XX	administration of a compound is used to inhibit formation of an					
PT	atherosclerotic lesion -					
XX						

This sequence represents the human AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

AA	Sequence	132 AA;
SQ		

Alignment Scores:

Pred. No.:	7.98e-11	Length:	132
Score:	174.50	Matches:	50
Percent Similarity:	32.67%	Conservative:	16
Best Local Similarity:	24.73%	Mismatches:	26
Query Match:	7.79%	Indels:	110
DB:	21	Gaps:	1

US-09-788-074-2 (1-1279) x AAY90320 (1-132)

QY	131	GGATAGGACTGCCTCTTAGAAGAATGGTGCCATGCCCAAGCCACACTGTATCATTCAG	190
		:: :: :: :: ::	
Db	25	GLyvaIClyPheAlathrArgLysValAlaGlyMetAlaLysProAsnMetIleIeSer	44
QY	191	TGTGATGGCAACAACATCATCGGTCAAACCAGGAGCAGCACAGTGAAGACGACTGTGTTCTCT	250

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85x2